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## Replacement Sheet

**Figure 1**

ID-65

Clone 3-60

5

(SEQ ID NO: 1)

GTGTTTATGAAAAAAAGGACAAGTAAATGATACTAAGCAA  
TCTTACTCTACGTAAATATAAATTGGTTAGCATCAGTAA  
TTTAGGGTCATTATAATGGTCACAAGTCCTGTTTGCAGGA  
10 TCAAACATCGGTTCAAGTTAATAATCAGACAGGCAGTAG  
TGTGGATGCTAATAATTCTCCAATGAGACAAGTGCCTCAAGT  
GTGATTACTTCCAATAATGATAGTGTCAAGCGTCTGATAAAAG  
TTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTC  
CTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTG  
15 AACAAAGGGATTATGTTATAGCAAAGAAACCGAGGTGAAAAA  
ATACACCTCAAAATCAGCCCCAGTAGCTTCTATGCAAAGA  
AAGGTGATAAAGTTTCTATGACCAAGTATTAAATAAAAGATA  
ATGTGAAATGGATTTCATATAAGTCTTGTTGGCGTACGTG  
ATACGCAGCTATTGAGTCAGTCCATCAGGAGGTTCA  
20 GACTAAAGCACCTACTCCTGTAACAAATTCAAGGAAGCAATAA  
TCAAGAGAAAATAGCAACGCAAGGAAATTATACATTTCA  
TAAAGTAGAAGTAAAAAATGAAGCTAAGGTAGCGAGTCAA  
CTCAATTACATTGGACAAAGGAGACAGAATTTCACGACC  
AAATACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAAATC  
25 ATTCAATGGTGTGTCGTTTGTAGGTAAAGCATCTT  
CAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAAC  
CACAAAGCCGTATTACTAAAACGGTAGACTGACTATTCTAA  
CGAAACAACTACAGGTTTGATATTAAATTACGAATATTAAA  
GATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTGGACTG  
30 AACAAAGGAGGGCAAGATGATATTAAATGGTATACAGCTGTA  
CTACTGGGGATGGCAACTACAAAGTAGCTGTATCATTGCTG  
ACCATAAGAATGAGAAGGGCTTTATAATATTCAATTAACTA  
CCAAGAACGACTAGGGACACTTGTAGGTGTAACAGGAAC  
AGTACAGTAGCTGGAACAAATTCTCTCAAGAACCTATTGA  
35 AAATGGTTACCAAAGACTGGTGTATAATATTATCGGAAGT  
ACTGAAGTAAAAAATGAAGCTAAAATATCAAGTCAGACCCAA  
TTTACTTTAGAAAAAGGTGACAAAATAATTATGATCAAGTA  
TTGACAGCAGATGGTACCAAGTGGATTCTTACAAATCTTATA  
GTGGTGTGTCGCTATATTCTGTGAAAAAGCTAACTACAAG  
40 TAGTAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTA  
TCCCAACTTACCTAAAACAGGTACCTATACATTACTAAA  
GTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCAGTGGAA  
TTAATTTCAAAAGGGTAAAAACATTATGATCAAGTGT

TAGTAGTAGATGGTCATCAGTGGATTCAACAGAGTTATT  
CGGTATTCTCGCTATATTGAAATTAA

5 (SEQ ID NO: 2)  
MFMMKKGVNDTKQSYSRKYKFLASVILGSFIMVTSPVFADQTSVQVNN  
QTGTSVDANNSSNETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETK  
PMVEKTLPEQGNYVYSKETEVKNTPSKSAPVAFYAKKGDKVFYDQVFVNKDN  
VKWISYKSFGGVRRYAAIESLDPGGSETKAPTPVTNSGSNNQEKIATQGNYT  
10 FSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIEGNQWLSYKSFGNVRRFV  
LLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTGFDILITNIKDDNGIA  
AVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNIHLY  
YQEASGTLVGVTKVTVAGTNSSQEPIENGLPKTGVYNIIGSTEVKNEAKISS  
15 QTQFTLEKGDKINYDQVLTADGYQWISYKSYSVRRYIPVKKLTSSEKAKD  
EATKPTSYPNLPKTGTYTFTKTVDVKSQPKVSSPVEFNFKGEKIHYDQVLVV  
DGHQWISYKSYSGIRRYIEI\*

Sequence description

- 20 A) Length: 1642 bp - 547 aa (full length gene)  
B) Sequence Characteristics:  
Potential leader peptide sequence  
Orf is preceded by a potential Shine-Dalgarno sequence.

25 ID-66

Clone 3-5

30 (SEQ ID NO: 3)  
ATGATATTGAGACGTCGAACTATTGTTTATGGCAACTGGGTATGCCATT  
TCTCTCATTCTTAGTATTCTAGCCTTAAATCTTATTCCATAGTACTCCCTT  
GCAAACCAATGCAGCTTACGGAACCTGCTCCTTCATTAAACCATCTTT  
TGGGACAGATGGTTAGGTAGGGATATGTTGTAGAACGATTAAAGGAC  
35 TTTATTCTCTACAAGTCGGCTTATTAGGTGCCCTATGGGGTCATTCT  
GGCGACAGTTTGGAGTGCTGCAGGTTAGGAAATAGCATTATTGATAA  
AATAATAGCATGGTTAGTGATTGTTATTGGTATGCCTCATTGATT  
ATGATTCTCATTCTTGTGGAAAGGTGCTCAAGGGTCATCATT  
GCAACGGCTGTTACACATTGGCCTTCTTAGCAAGGCTTATCCGAATGAA  
40 GTCTATCATCTAAAGAATAAAGAATTGTCCAACCTTCTAAAAGTATGGGA  
AAAACGCCTTATTATATTGTGAGGCATCATCCTGCCTTGATTGCTTCTC  
AAATTTCATTGGTTTATCCTCTTATTCCACATGTCATCCTACATGAAGC  
ATCAATGACTTCTTAGGATTGGCTCTGCCGAACAAACCTCGGTTGG  
TATCATTCTGTCAGAGGCAGCTAACATCTCTTGGAAATTGGTGGTT

GGTTATCTTCCAGGACTTATCTTATTGGTTGTCAATGCATTGATACT  
ATCGGAGAATCTTAAAGAACTCTTACCCCTCAAACGTGATCATTAG

5 (SEQ ID NO: 4)

MILRRRTIVLWQLGIAISLILSILALNLYFHSTPLQTNAALRNLAPSLNHLFGTD  
GLGRDMFVRTIKGLYFSLQVGVLGALMGVILATVFGVLAGLGNSIIDKIIAWL  
VDLFIGMPHLIFMILISFVVVGKGAQGVIIATAVTHWPSLARLIRNEVYHLKNKE  
FVQLSKSMGKTPYYIVRHILPLIASQIFIGFILLFPHVILHEASMTFLGFGLSAE  
10 QPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTIGESLKKLFYPQTDHF  
\*

Sequence description

15

A) Length: 822 bp - 274 aa (full length gene)

B) Sequence Characteristics:

Potential leader peptide sequence

20

Orf is preceded by a potential Shine-Dalgarno sequence.

ID-78

25

Clone 3-5b

(SEQ ID NO: 5)

ATGACAGAACATTATTAAGCATTAAAGACCTCTCCATCACCTCACTCAA  
TACGGAAGATTTAAAACCATTCAATCAACACCGATAACAAGCGCTGA  
30 ATTTAGAAATTAAAAAGGTGAGTTATTAGCTATTAGGTGCTAGTGGTT  
CGGGGAAGAGTTATTAGCACATGCTATTATGGATATTCTCCTAAAAATG  
CATCTGTAACAGGAGATATGATTATCGTGGTCAATCACTAAATTCTAAAC  
GCATTAAACAGTTGCGAGGAAAAGATATTACGTTGATTCCACAATCAGTT  
AATTATTTAGATCCATCTATGAAAGTCAAACATCAGGTGCGCTTAGGTATC  
35 TCAGAAAATTCAAAGGCTACTCAAGAAGGATTGTTCAACAGTTGGTTA  
AAAGAAAAGTGTGGACTTGGATCCTTCCAACTTCTGGCGGAATGCTC  
CGACGTGTTGTTACAACGTGTATTAGTGATAAGGTTCTTGATTATTG  
40 CGGATGAGCCCACCCCTGGATTACATCCAGATGCTCTGCAAATGGTTTAG  
ACCAACTACGCTCCTTGCAGATAAAGGAATAAGCGTTATATTACTCAGT  
ATGATATTGTAGCAGCTAGTCAAATTGCTGATCGTATTACTATTAAAG  
AGGGAAAAGCTATTGAAACAGCTCCAGCTAGTTCTTAGCGGAAATGGA  
GAGCAGTTACAAACAGAATTGCTAGAAGTTATGGCGCTCTCTCCCACAG  
CAAGAATTGGAAAGGAGTTACTCATGACCTTAGAGGCTAA

(SEQ ID NO: 6)

MTETLLSIKDLISITFTQYGRFLKPFQSTPIQALNLEIKKGELLAII GASGSGKSLL  
AHAIMDILPKNASVTGDMIYRGQSLNSKRIKQLRGKDITLIPQS VNYLDPSMK  
VKHQVRLGISENS KATQEGLFQQFGLKESDG DLPFQLSGGMLRRVLFTTCIS  
DKVSLIIADEPTPGLHPDALQMVL DQLRSFADKG ISVIFITHDIV AASQIADRITI  
FKEGKAIETAPASFFSGNGEQLQTEFARSLWRS LPQQEFLKG VTHDLRG\*

5

10 Sequence description

A) Length: 804 bp - 268 aa (full length gene)

B) Sequence Characteristics:

No obvious leader peptide sequence

15 Orf is preceded by a potential Shine-Dalgarno sequence.

This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was

20 identified downstream and fully sequenced.

ID-79

25 Clone 3-5c

(SEQ ID NO: 7)

GTCCATCTGGGGTGGTCCCGATTGGTATTCTTCTCCGATAGGTACTTG A  
GTCAAGATATTACGTTAGCTGATCGTATTAAGCACCTTATT TACCTGTTT  
30 CACGGTAAGTATTCTAGGCATTGCCAATGTA ACTCTTCATACTAGAACTAA  
AATGATGTCGGTACTTTCTAGTGAATATGTCTATTGCCAGAGCGCGTGG  
GGAAACGGAATGGCAAATT TAAAAATCATTGTCTTAGAAATGCTATCGT  
ACCAGCTATTACACTGCATT TT CCTATTGGAGAATTGTTGGAGGATCC  
GTTCTGCTGAGCAAGTTCTCATATCCAGGACTAGGGTCTACCCTAACT  
35 GAAGCAGGACTTAAAAGT GATA CACCGCTACTTCTAGCTATTGTGATGATA  
GGGACATTATTGTTTGC GGGCAATCTATTGCGGATATT TAAATAGC  
ATAATCAATCCACAGTTAAGGAGAAAAGTATGA

(SEQ ID NO: 8)

40 VHLGWFPIGISSPIGLSQDITLADRIKHLILPVFTVSILGIANVTLHTRTKMMSV  
LSSEYVLFARAR GETEWQIFKNHCLRNAIVPAITLHF SYFGELFGGSV LAEQVF  
SYPGLGSLTEAGLKSDTPLLLAIVMIGTLFVFAGNLIADILNSIINPQLRRKV\*

Sequence description

A) Length: 495 bp - 165 aa (partial gene sequence)

B) Sequence Characteristics:

N-terminus has yet to be determined.

5 This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified upstream.

10

ID-80

Clone 2-17

15 (SEQ ID NO: 9)

TTGCGGACAATTACGTTCAAACACAATGAAACCGCGATCGTCAAAAAGCGA  
AGGTAGGGCGGTAATGCTAAAAGATTATTACTGAAGATGGGGATTGA  
CAAAGATTAGTCGTCGTTGGATGTTAGTGGTTATCTATTGTCTTAT  
TATTGTCAGGATGTGTTGGGCCTCAAATTATGATTGAGGGGGTATCAAC  
20 TCCGAATGTTAGCGCTTCGGAAGAATTGTAGCTCTTAGTACCATTTAA  
TTCTTTCTGAGTTAGATCAGCTAACTAGCTTAAAGAGATTGGGGTT  
ATTGGTCAAAATGTAGTGAATATTACTGCTGTTCCCTCTCATTATAGGGT  
TACTATCCCTAAAGCCAAGTTACGGAAATATAAAAGCGTTATATTACTG  
CTTTCTTGATGTCTCTTCATAGAGTGTACTCAAGTTAGATATT  
25 AATAGATGCTAACGGGTTTGAAATCGACGATCTATGGACAAATACCTT  
AGGCGGTCTTCGCCCTATGGAGTTATCGAACATAAAAGGTTGGCTCT  
AACTATTAGAAAATGA

(SEQ ID NO: 10)

30 MRTITFKHNETRSSKSEGRAVMLKRLFTEDGELTKISRRFVWMLVVIYCLIIVR  
MCFGPQIMIEGVSTPNVQRFRGRIVALLVPFNSFRSLDQLTSFKEIFWVIGQNVV  
NILLLFPLIIGLLSLKPSLRKYKSVILLAFLMSLFIETQVVLDILIDANRVFEIDD  
LWTNTLGGPFALWSYRNIKGWLLTIRK\*

35

Sequence description

A) Length: 579 bp - 193 aa (full length gene)

B) Sequence Characteristics:

40 Possesses a potential leader peptide sequence  
No obvious Shine-Dalgarno, but the 'TTG' codon may not be the actual translation start point.  
A methionine (ATG) that occurs ~22 codons downstream of the 'TTG' is preceded by a

potential Shine-Dalgarno sequence and may represent the actual start codon.

ID 81

5

Clone 3-1

(SEQ ID NO: 11)

TTGAAAAATTAAATCGTTATGTAGTTGGAGTCGTTTACATT  
TAATGCTAGGATCAACTATGCTGGAGTGTGTTCGTAACCCAATTATCT  
CAGAGACTGGTGGGATATTCATCAGTTCATTGCTTTAGTTGGCTAT  
TTTTGTCTAGGAATGTCAGCTTTATGGGACACTTAGTAGAGCGTTT  
GGCCTAGGATAATGGGAATGATTCTGCTATTATGGAGCAGGAAAT  
GTGTTAACAGGCTTAGCCATTGAAAATCAGCAGTTATGGTTACTGTATGTT  
GCATACGGTATTTAGGAGGAATCGGACTTGGTCAGGTTATATTACTCCA  
GTATCGACTATTATTAAATGGTTCTGATAGGAGGGGACTAGAACACAGG  
ATTCGCTATTATGGGATTGGCTTCTTAGTAACAAGTCCGCTTGCA  
CAATCCTACTGATTAGGATTGGTGTGGTAAAACGTTTATATTGGGA  
TTAGTATATTTTTGTCATGATGATTGCCTCACAAATTATTAAACAACCAC  
CTCAGGAAAAAAATAACTATTTGACTCACGATGGTAAAAAGAATGCTATG  
AATTACAAAATTACTGGATTAAAAGCAAACGTCGCTATAAAATCAA  
AACCTTTACATCATTGGTGACCTGTTATTAAATATTCTGTGGCTTA  
GGTTAATATCAGCAGCTCACCAATGGCACAAGATTAGCAGGCTATTCC  
GCAGAATCTGCAGCCTTATTAGTAGGGGACTAGGGATATTAAACGGTTT  
GGACGTCTGTTATGGCAAGTCTCTGACTACATTGGACGCCGTTGACC  
TTTATAATATTATTGTGAACTTATTATGACTTCTAGTTATTGTC  
ATTCAATGCTATTGTATTGCAATAGCGATGTCTATTAAATGACTTGTAT  
GGTGCAGGTTTCCTTATTACCTGCTTATCTAAGTGATATTGGAAACAA  
AGGAATTAGCTACTTACATGGTTAGTTAACAGCATGGCAATAGCAG  
GTCTGTTGGGCCCTATTGTTATCAAAGACATATTGACGGATTATTGTTA  
ATCAATTGACATTAATGGTTTGGTTTATTCTTATTGGATTATTGTTA  
TCTCTATATTAAAGAAAATTAAACAACAAAGTTGTGTAG

(SEQ ID NO: 12)

35 LKNLNRYVVAVSGVVLHMLGSTYAWSVFRNPIISETGWDISSLFAFSLAIFC  
LGMSAAFMGHLVERFGPRIMGMISAILYGAGNVLTGLAIETQQLWLLYVAYG  
ILGGIGLGSYITPVSTIWKFPDRRGLATGFAIMGFGFASLVTSPAQSLLIRIG  
VGKTFYILGLVYFFVMMIASQFIKQPPQEKITILTHDGKKNAMNSQIITGLKAN  
VAIKSKTFYIWLTLFINISCGLGLISAASPMQAQDLAGYSAESAALLVGVLGIN  
40 GFGRLLWASLSDYIGRPLTFIILFIVNFIMTSSLFLSFNAIVFAIAMSILMTCYGA  
GFSLLPAYLSDIFGTKELATLHGYSLTAWAIAGLFGPLLSKTYSWGNSYQLTL  
MVFGFLFLFGLLLSLYLRKLTTKVV\*



Sequence description:

- 5            A] Length 1221 bp - 407 a.a (full length gene).  
              B] TTG start codon with Shine-Dalgarno sequence upstream. Obvious signal peptide, with hydropathy plot exhibiting many possible membrane spanning regions, indicating protein to be transmembrane.
- 10
- ID-82
- Clone 48
- 15            (SEQ ID NO: 13)  
ATGGCAGATAAAAACAGAACATTAAACTTGTAGGTGCAGGATCTTCTAG  
CACACAAGAAAAAAATTGAAAAGCCTGCTCTTCGTTATGCAAGATGCGTG  
GCGTCGCTTGAAAAAAAACAAATTAGCAGTAGTTCACTCTATTATTAGC  
20            TCTTTACTTACTTTCTGTTAGCCTCAAATTATTGTAACTCAGAAGGAT  
GCTAATGGGTTGATTGAAAAAGTAACGACATATCGCAACTTACCACCT  
AAATTGAGTTCAAACCTCCTTTGGAATGGTAGCATTAATCCATCA
- (SEQ ID NO: 14)  
25            MADKNRTFKLVGAGSSSTQEKIEKPALSFMQDAWRRRLKKNKLA  
LLLTFSLASNLFVTQKDANGFDSKKVTTYRNLPKLSSNLPFWNGSINPS

Sequence description:

- 30            A] Current length is 303 bp - 101 aa  
              B] No obvious signal peptide but Shine Dalgarno sequence upstream of the ATG start codon. Not identified directly using the LEEP system but was found directly downstream of ID-34 described in WO 00/06736.

ID-83

- 40            Clone 98
- (SEQ ID NO: 15)  
ATGAAAATAGTAGTACCACTAGTAATGCCTCGCAGTCTTGAAGAGGGCTCAAGA  
AATAGATTATCAAAATTGATAGTGTGATATTATTGAATGGCGAGCTGA

TGCCTTACCAAAAGGATGACATTATTAATGTAGCTCCAGCTATTTGAGAA  
ATTCGCAGGTATGAAATTATTTACTTTCGTACAACCGGTGAAGGTGG  
TAATATTGTCTTATCTGATGCTGAGTATGTTGAGTTAACAGAAAATTAA  
5 TTCTATCTACAATCCAGATTATGATTGAGTATTTCACATAAAGAA  
GTTTTCAAGAAATGCTAGAATTCCAAATTAGTCCTGTCTTACAAATT  
TTCAAGAGACACCGGAGAATATTATGGAGATATTCAGAACATTACAGCC  
CTAGCACCACGAGTTGTGAAAATCGCAGTAATGCCAAAGAACATGAACAAGA  
TGTCTTAGACGTTATGAATTACACTCGCGGTTCAAGACTATTAATCCTGA  
10 TCAAGTTATGCGACGGTATCTATGAGTAAAATTGGACGTATTCTCGTTT  
GCTGGTGATGTAACGGATCTAGTTGGACATTGCATATTAGATTCATCT  
ATCGCACCCGGACAAATTACTATTCAGAGATGAAGCGTGTCAAAGCATT  
GCTTGACGCTGACTGA

(SEQ ID NO: 16)

MKIVVPVMPRSLEEAQEIDL SKFDSVDIIEWRADALPKDDIINVAPAIFEKFAG  
HEIIFTFR TTREGGNIVLSDAEYVELIQKINSIYNPDYIDFEYFSHKEVFQEMLEF  
PNLVLSYHNFQETPENIMEIFSELTALAPRVVKIAVMPKNEQDVLDVMNYTRG  
FKTINPDQVYATVSMSKIGRISRFAGDVTGSSWTFA YLDSSIAPGQITISEMKRV  
KALLDAD\*

20

Sequence description:

A] Length 678 bp, 225 aa (full length gene)

25

B] No obvious signal peptide, but there is a  
Shine Dalgarno immediately upstream of ORF.

ID-84

30

Clone RS-52

(SEQ ID NO: 17)

ATGAAAGACTTATTGCAACAAACAGAACATCATCAAGGAAACAGGAACA  
AGATAGAATTGTCAATTACATAAAACACATGTTGAGTTAACAAATGGTA  
35 ATCAAATAAAAAAAATTGAGTTATCGACTTTCAAAAAAATGAGATGACA  
GGTACATGGGAATTCTACTAAATGAACAATTTCGATTAGTTT  
TCTGAAGATAGAATTGGTGGTAAACTAGAGCATTAGGATATCAACCGAA  
40 TGAAATAGGTTTCAAAGGACATCAATAGTAATAATCAAAATGTTAATGA  
TATTGAAGTGATTATGAAGAAAGAATAG

(SEQ ID NO: 18)

MKDLFATTEASSRKQEQRIVNYIKQHVELTNGNQIKKIEFIDFQKNEMTGTW  
GISTKINEQFSISFSEDRIGGKLRALGYQPNEIGFSKDINSNNQNVNDIEVIYMK  
KE\*

5

Sequence description:

A] length: 333 bp - 111 aa (partial sequence)

10 B] No obvious Shine Dalgarno sequence upstream  
of the ATG start codon, and no obvious signal  
peptide within the protein.

ID-85

15

Clone RS-53

(SEQ ID NO: 19)

20 ATGAAAAAAACGTATATGGTATTGATAATAATAATCACAGTAATTAGGA  
GGACTAGCCATGAAAAACTTATTGCAACAACAGAAGCATCATCAAGGAA  
ACAGGAACAAGATAGAATTGTCAATTACATAAAACAACATGTTGAGTTAA  
CAAATGGTAATCAAATAAAAAAAATTGAGTTATCGACTTCAAAAAAAAT  
GAGATGACAGGTACATGGGAATTCTACTAAAATTAAATGAACAAATTCG  
ATTAGTTTCTGAAGATAGAATTGGTGGTAAACTAGAGCATTAGGATAT  
25 CAACCGAATGAAATAGGTTTCAAAGGACATCAATAGTAATAATCA

(SEQ ID NO: 20)

30 MKKRIWYLIIITVILGLAMKNLFATTEASSRKQEQRIVNYIKQHVELTNGN  
QIKKIEFIDFQKNEMTGTWGISTKINEQFSISFSEDRIGGKLRALGYQPNEIGFSK  
DINSNNQ

Sequence description:

35

A] Length: 351 bp - 117 aa (Partial sequence)

B] Obvious signal peptide and Shine Dalgarno  
sequence upstream of the ATG start codon.

40

ID-86

Clone ID-74

(SEQ ID NO: 21)

ATGTCAAATCAATATGATTATATCGTTATTGGTGGAGGTAGT  
GCAGGCAGTGGTACCGCTAATAGGGCAGCCATGTATGGAGC  
AAAAGTCCTGTTAATTGAAGGTGGACAAGTAGGTGGAACCTG  
5 TGTTAACTTAGGTTGTACCTAACGAAAATCATGTGGTATGG  
TGCACAAGTTCTGAGACACTCCATAAGTATAGTCAGGTTA  
TGGTTTGAGCCAATAATCTTAGTTGATTTACTACTCTA  
AAAGCTAACCGCGATGCTTACGTGCAGCGGTCTAGACAGTCG  
TATGCCGCTAATTTGAGCGTAATGGGGTCGAAAAGATTGAT  
10 GGATTGCTCGTTATTGATAACCATACTATTGAAGTGAATG  
GTCAGCAATATAAAGCTCCTCACATTACTATTGCAACAGGTG  
GACACCCTCTTACCCCTGATATTATTGGAAGTGAACTTGGT  
AGACTTCTGATGATTTGGATGGAGACCTTACCAAATT  
TATATTGATTGTTGGGGCGGGCTATATCGCGGCAGAACTTGC  
15 TGGAGTGGTTAATGAATTAGGCCTGAAACCCATCTTGCATT  
TAGAAAAGACCATATTCTACCGCGATTGATGACATGGTAAC  
AAGTGAGGTTATGGCTGAAATGGAGAAATCAGGTATCTCTT  
ACATGCTAACCATGTACCTAAATCTCTAAACCGCGATGAAGG  
TGGCAAGTTGATTTGAAGCTGAAAATGGAAAACGCTTGT  
20 CGTTGATCGTGTAAATATGGGCTATCGGCCGTGGACCAAATGT  
AGACATGGGACTTGAAAATACCGATATTGTTAAATGATAA  
AGATTATATCAAAACAGATGAATTGAGAATACTTCTGTAGA  
TGGCGTGTATGCTATTGGAGATGTTAATGGAAAATTGCCTT  
GACACCGGTAGCAATTGCAGCAGTCGCTTATCAGAAAG  
25 ACTTTTAATCATAAAGATAACGAAAAATTAGATTACCAAA  
TGTACCTTCAGTTATTTACTCACCCCTGTAATTGGGACGGTA  
GGACTTTCAGAACGCAGCAGCTATCGAGCAATTGGAAAAGAT  
AATATCAAAGTCTATACATCAACTTTACCTCTATGTATACGG  
CTGTTACCAAGTAATGCCAAGCAGTTAAGATGAAGCTCATAA  
30 CCCTAGGAAAAGAGGAAAAAGTTATTGGCTCATGGTGTG  
GTTATGGTATTGATGAAATGATTCAAGGTTTCAGTTGCTAT  
CAAAATGGGGCTACTAAAGCAGACTTGATGATACTGTTGC  
TATTCAACCAACTGGATCTGAGGAATTGTTACAATGCGCTA  
A  
35

(SEQ ID NO: 22)

MSNQYDYIVIGGGSAGSGTANRAAMYGAKVLLIEGGQVGGTC  
VNLGCVPKKIMWYGAQVSETLHKYSSGYGFEANNLSFDFTTLK  
ANRDAYVQRSRQSYAANFERNGVEKIDGFARFIDNHTIEVNGQ  
40 QYKAPHITIATGGHPLYPDIIGSELGETSDDFFGWETLPNSILVG  
AGYIAAELAGVVNELGVETHLAFRKDHILRGFDDMVTSEVMAE  
MEKSGISLHANHVPKSLKRDEGGKLIFEAENGKTLVVDRVIWAI  
GRGPNVDMGLENTDIVLNDKDYIKTDEFENTSVDGVYAIGDVN  
GKIALTPVAIAAGRRLSERLFNHKDNEKLDYHNVPSVIFTHPVIG

TVGLSEAAAIEQFGKDNIKVYTSTFTSMYTAVTSNRQAVKMKLI  
TLGKEEKVIGLHGVGYGIDEMIQGFSVAIKMGATKADFDDTVAI  
HPTGSEEFVTMR\*

5

ID-87

Clone RS-55

10 (SEQ ID NO: 23)  
ATGACAAAAAAACATCTTAAAACGCTTGCCTGGCACTTACTACAGTATCA  
GTAGTGACATACAGCCAGGAGGTATATGGATTAGAAAGAGAGGAATCGGT  
CAAACAAGAACAAACCCAGTCAGCTTCAGAAGATGATTGGTTCGAAGAAG  
ATAATGAGAGGAAAACAAATGTTCTAAAGAGAATTCTACTGTTGATGAA  
15 ACAGTTAGTGATTTATTTCTGATGGAAATAGTAATAACTCTAGTTCTAAA  
ACCGAGTCAGTGGTAAGTGACCTAAACAAAGTCCCCAAAGCAAAACCAGA  
GGTTACACAAGAAGCAAGCAATTCTAGTAATGATGCTAGCAAAGTAGAAG  
TACCAAAACAGGATACAGCTCAAAAAAGGAAACTCTAGAAACATCAACT  
20 TGGGAGGCAAAAGATTCTGTAACTAGAGGGGATACTTAGTAGGTTTTCA  
AAATCTGGAATTAATAAGTTATCTCAAACATCACACTGGTTTACCAAGT  
CATGCAGCAGATGGAACTCAATTGACACAAAGTAGCTAGCTTGCTTTACT  
CCAGATAAAAAGACGCCATTGCAGAATATACAAGTAGGCTAGGAGAAA  
ATGGGAAACCGAGTCGTTAGATATTGATCAGAAGGAAATTATTGATGAG  
GGAGAAATATTAATGCTTACCAAGTTGACTAAGCTTACTATTCAAATGGT  
25 TATAAGTCTATTGGTCAAGATGCTTTGTGGACAATAAGAATATTGCTGAG  
GTTAACCTTCCTGAGAGTCTCGAGACTATTCAGACTATGCTTTGCTCACA  
TGTCTTAAAACAAGTAAAGTTACCAAGATAACCTAAAGGTCAATTGGAGAA  
TTAGCTTTTTGATAATCAGATTGGTGGTAAGCTTACTTGCCACGTCACT  
TGATAAAAATTAGCAGAACCGCTTCAAATCTAATCGTATTCAAACAGTTG  
30 AATTTTGGGAAGTAAGCTTAAGGTTATAGGAGAAGCAAGTTTCAAGAT  
AATAATCTGAGGAATGTTATGCTTCCGGATGGACTTGAAAAAAATAGAATC  
AGAAGCTTTACAGGAAATCCAGGAGATGAACATTACAACAATCAGGTTG  
TATTGCGCACAGGACAGGCCAAATCCACATCAAACATTGCGACTGAGAAT  
ACTTACGTCAATCCGGACAAATCATTGTGGCGTGCAACACACCTGATATGGAT  
35 TATACCAAATGGTAGAGGAAGATTACCTATCAAAAAAAATAGTGTACA  
GGTTTTCAAATAAAGGCTTACAAAAGGTAAAGACGTAATAAAAAACTTAGA  
AATTCCAAAACAACACAATGGTATTACTATTACTGAAATTGGTGATAACGC  
TTTCGCAATGTTGATTTCAGGAAACTTACGTAAATATGATTGGAA  
AGAAATAAAGCTCCCCTCAACTATTGGAAAATAGGTGCTTTGCTTTCA  
40 ATCTAATAACTGAAATCCTTGAAGCAAGTGAAGATTAGAAGAGATTA  
AAGAGGGAGCCTTATGAATAATCGTATTGGAACCTAGACTTGAAAGAC  
AAACTTATCAAATAGGTGATGCTGCTTCCATATTAATCATATTATGCC  
ATTGTTCTCCAGAATCTGTACAAGAAATAGGACGTTAGCTTACGACAA  
AATGGTGCGCTTCACCTATGTTATCGGAAATAAGGTAAAACAATTGGT

GAAATGGCTTTTATCCAATAACTGGAAAGTGTAAATCTCTCTGAGCAA  
AAACAATTAAAGACAATTGAGGTCCAAGCTTTCGGATAATGCCCTAGT  
GAAGTAGTCTTACCGCCAAATTACAGACTATTCTGAAAGAGGGCTTC  
AGGAATCATTGAAAGAAGTGAAGGGTCATCTACATTATCTCAGATTACT  
5 TTTAATGCTTTGATCAAAATGATGGGGACAAACGCTTGTAAGAAAGTG  
GTTGTTAGGACACATAATAATTCTCATATGTTAGCAGATGGTGAGCGTT  
ATCATTGATCCAGATAAGCTATCTTCTACAATGGTAGACCTTGAAAAGGTT  
TTAAAAAATAATCGAAGGTTAGATTACTCTACATTACGTCA  
ACTCAGTTAGAGAAATGACTACTGCAGGTAAAGCGTTATCAA  
10 AACCTCCGACAAGGAGAAAAACAAAAATTCTCAAGAACAGACAATT  
CCTTGGTCGCGTTGATTGGATAAAGCCATAGCTAAAGCTGAGAACGGCTT  
AGTACCAAGAACGAAAGAACAAAGAACATGGTCATTGCTGAGAGGAGTATT  
ACAAAGCGGTATTAGCTTATAATAATAGTGTATTAAAAAGCTAATGTTA  
AGCGCTTGGAAAAAGAGTTAGACTTGCTGACAGATTAGTCGAGGGAAAA  
15 GGACCATTAGCGCAAGCTACAATGGTACAAGGAGTTATTAAAGAC  
GCCTTACCATGCCAGAATATTATATCGGATTGAACGTTATTGACAA  
GTCTGGAAAATTGATTATGCACTTGATATGAGTGTACTATTGGCGAGGG  
ACAAAAAGATGCATATGGTAATCCTATATTAAATGTTGACGAGGATAATG  
AAGGTTATCATACTTGGCAGTTGCCACTTAGCTGATTATGAAGGTCTT  
20 ATATTAAAGATATTAAATAGTCCCTGATAAGATTAAAGCAATACGCC  
AGATTCCCTTGGCAAAATATCATAGATTAGGAATTTCAGCTATCCGAA  
ATGCAGCGGCAGAACGACCGATTGCTCCTAACAGACACCTAACGGGTAC  
CTAAATGAAGTCCCATTATCGTAAAAAACAAATGGAGAAAAATTAAA  
ACCAGTTGATTATAAAACGCCATTAAATAAGGCTTACCTAACGAA  
25 GGTAGACGGTGTAGAGCGGCTAAAGGTCTAACATATAATGCGGAGACTA  
ATAATTCTGTAGCTGTAACACCAATAAGGTCCGAGCAGCAATTACATAAGT  
CACAGTCTGATGTAATTACCTCAAACAAGTTCTAAAAATAATTTATAT  
ACGAGATTCTAGGATACGTTAGTTATGTTGCTTCTAGTAACGCTGG  
GAAAAAAAGGAAAACGAGCAAGAAAATAA  
30 (SEQ ID NO: 24)  
MTKKHLKTLALALTTSVVTVSQEVYGLEREESVKQEQTQSASEDDWFEEDN  
ERKTNVSKENSTVDETVDLSDGNSSNSKTESVVSDPKQVPKAKPEVTQE  
ASNSSNDASKVEVPKQDTASKKETLETSTWEAKDFVTRGDTLVGFSKGINKL  
35 SQTSHLVLPSHAADGTQLTQVASFAFTPDKKTAIAEYTSRLGENGKPSRLDIDQ  
KEIIDEGEIFNAQQLTKLTIPNGYKSIGQDAFVDNKNIAEVNLPELETISDYAF  
AHMSLKQVKLPDNLKVGELAFFDNQIGGKLYLPRHLIKLAERAFKSNRIQTV  
EFLGSKLKVGIEASFQDNNLRNVMLPDGLEKIESEAFTGNPGDEHYNNQVVL  
TRTGQNPHQLATENTYVNPDKSLWRATPDMDYTKWLEEDFTYQKNSVTGES  
40 NKGLQKVRRNKNLEIPKQHNGITITEIGDNAFRNVDFQSRTLKYDLEEIKLPS  
TIRKIGAFAFQSNNLKSFEASEDLEEIKEGAFMNNRIGTLDLKLIKIGDAAFH  
INHIYAIVLPEVQEIGRSAFRQNGALHLMFIGNKVKTIGEMAFLSNKLESVNL  
SEQKQLKTIEVQAFSDNALSEVVLPPNLQTIREEAFKRNHLKEVKGSSTLSQITF  
NAFDQNDGDKRGKKVVVRTHNNSHMLADGERFIIDPDKLSSTMVDLEKVL

KIIEGLDYSTLRQTTQTQFREMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGR  
VDLDKAIAKAEKALVTKKATKNGHLLERSINKAVLAYNNSAIKKANVKRLEK  
ELDLLTDLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  
5 LDMSDTIGEGQKDAYGNPILNVDEDNEYHTLAVATLADYEGLYIKDILNSSL  
DKIKAIRQIPLAKYHRLGIFQAIRAAAEDRLLPKTPKGYLNEVPNYRKQM  
EKNLKPVDYKTPIFNKALPNEKVDGDRAAKGHNINAETNNSAVTPIRSEQQL  
HKSQSDVNLPQTSSKNNFIYEILGYVSLCLLFLVTAGKKGKRARK\*

10 Sequence description:

- A] Length 3168 bp - 1056 aa (Partial sequence)
- B] Obvious signal peptide with Shine Dalgarno sequence upstream of the ATG start codon.

15

ID-88

20 Clone RS-56

(SEQ ID NO: 25)

GCAGGATACATCATGCACAAGCACGAGGCTATCGTGTATGCTGGGTCA  
ACCCAGGAAGACATGTCGGCACAAAGCTGAAGATTCTTACAGTCTGTACA  
25 CAATAAAGAGACGGGTAAGAGAGCGCTTTAACATGACAAAGAACGACTAGCAA  
TT

(SEQ ID NO: 26)

AGYIMHKHEAIVSCWGQPRKTCRHKLKISLQS VHNKETGKSAFNDKERLAI

30

Sequence description:

- 35
- A] Length:153 bp - 51 aa (partial sequence)
  - B] No signal peptide visible, insufficient sequence data to determine the presence of a Shine Dalgarno sequence.

40 ID-89

Clone RS-58

(SEQ ID NO: 27)

GTGTCATTATGCAAAGAAAATCCTATTAAAATCCATGAGTGTCTTACT  
TTAACAGCTTGTCTTATATCAGGATATGTGGTTAAAGATATTGCTATGTTA  
CATGCAGTATCTGCCAGTGAGAAGAAAGCAAATAATGTCAGTCCGAGAGA  
5 AAATCTCTACAGGGCTGTCAATGATAATTGGCTAGCCAATACAAAAACTCA  
AACAAAGGGCAGACTAGTGTAAATAGTTTTCAGAAATTGAGGATAAATTAA  
AAGCAACTGTTAGTGTCTGATATGGCTAAAATGGCCTCAGGAAAGATTGA  
AACAAACCAATGATGAACAGAAAAAAATGGTGCATACTATAAACAAAGGTAA  
TGGACTTTAAAACAAGAGATAAAAATGGTCTCAAACCTCTAAAACCAGTT  
10 TTACAAAAACTTGAAGCAGTCTCTCAATGAAAGACTTCAAAGTTGGCC  
CATGATTTGTGATGAGTGGTTTGTGTTACCATTTGGTTGACTGTGGAAA  
CCAATGCTCGAGATAATAGCCAAAAGCAATTGGTGCCTCGTCAAGCACCC  
GCATTACTTGAATCACCTGACCAATATAAGAAGGGCAATAAAGAAGGTGA  
GGCTAAATTATCAGCTTACCGTACTTCAGCAATGGCTTGCTTAAACAAGC  
15 TGGAAAAAGTAACATTGAAGAGATAAGAAAAACTAGTTAAACAAGCTATAGCAT  
TTGATAGACTCTTATCAGAAAAACGCAAGTTGATCAAAGTAAAATCACA  
GCTGAAAGTGAGACAGCTGCGGGCGATATAACCCTGAAAGTATGGAAAC  
GGTTCACAAATTACGCCAAGGAATTGACTTTAAAGAATTGATTGAAAAACT  
AGTTGGGCCAACGAATAAGGCAGTCAATGTAGAAGAGATAAAACTTATTTA  
20 AACAGGTTAATGATGTTATAAAATAGTAAACAATTAGCCAATATGAAAGCA  
TGGATGATGATTCTATGCTAGTTGATCAATCAGATTCTAGGAGAACAA  
AATCGTCAAGCAGCGAGTGCTTTAAGAATGTTGCGTCTGGTTGACTCAG  
ATTGAATCGAAAGAAAAATGCTTACACCCAATTAG

25

(SEQ ID NO: 28)

MSFMQRKSYLKSMsvltLTACLISGYVVKDIAMLHAVSASEKKANNVSPREN  
LYRAVNDNWLANTKLKQGQTSVNSFSEIEDKLKQLLVSDMAKMASGKIETTN  
30 DEQKKMVAYYKQGMDFKTRDKNGLKPLKPVLQKLEAVSSMKDFQSLAHDF  
VMSGFVLPFGLTVETNARDNSQKQLVLRQAPALLESQDQYKKGNKEGEAKLS  
AYRTSAMALLKQAGKSNIEDRKLVKQIAFDRLLEKTQVDQSKITAESSETAA  
GRYNPESMETVHNYAKEDFKELIEKLVGPTNKAVNVEDKTYFKQVNDVINS  
KQLANMKAWMMISMLVDQSDFLGEQNRQAASAFKNVASGLTQIESKEKMLT  
PN\*

35

Sequence description:

40

- A] Length: 1095 bp - 365 aa (full-length gene)
- B] an GTG (possible ATG start codon located 7 bp further downstream) start codon with an obvious signal peptide. Shine Dalgarno sequence present upstream of the ORF.

ID-90

Clone RS-59

5

(SEQ ID NO: 29)

ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTAAAATGAG  
TATTGATAAACTTAGATATAAAGAACCAAGAGAGTGAACATGACAAGCGAC  
CTACTTTTATTGGTAGTACTTATACTGTTACTGTAGCAGTTATATTGTC  
10 GTTATTAAATATTTTATAG

10

(SEQ ID NO: 30)

MEMPKRNELLNKEIKMSIDKLRYKEPESEHDKRPTFYLVVLILVTVAVILSLFK  
YFL\*

15

Sequence description:

20

A] Length: 174 bp - 58 aa(full length gene)

B] No obvious signal peptide, but Shine

Dalgarno sequence is present upstream of ATG  
start codon.

25

ID-91

Clone RS-62 (partial sequence)

30

(SEQ ID NO: 31).

ATGCAGGTATTTAAATATTGTCAATAAATTCTTGATCCAGTTATTCATA  
TGGGTTGGGAGTTGTGATGCTAATTGTCATGACAGGTTAGCCATGATAT  
TTGGAGTGAAGTTCTAAAGCACTTGAAGGTGGTAT

35

(SEQ ID NO: 32)

MQVFLNIVNKFFDPVIHMGSGVVMLIVMTGLAMIFGVKFSKALEGG

Sequence description:

40

A] Length:141 bp - 41 aa (partial sequence

B] Shine Dalgarno sequence present upstream of  
ATG start codon with a possible signal peptide  
present



ID-92

5      Clone RS-69 (partial sequence)

(SEQ ID NO: 33)

ATGAAAAAAGAAAACATTCACTGCTTATAACTTTAACGGCTCTTATCCTT  
10      TGTCTTTGACAGTGCTTTATCTTCCATTATTGGATTATGACAGGAG  
CTTTAA

(SEQ ID NO: 34)

MKKKTFSAYNFLTALILCLLTVLFIFPFYWIMTGAF

15

Sequence description:

A] Length: 110 bp -36 aa (Partial sequence)

20

B] Possible signal peptide with Shine Dalgarno  
sequence directly upstream of the ATG start  
codon.

25

ID-93

Clone RS-70

(SEQ ID NO: 35)

30

ATGACTGAGAACTGGTTACATACTAAAGATGGTCAGATATTATTATCGT  
GTCGTTGGTCAAGGTCAACCGATTGTTTTACATGGCAATAGCTTAAGT  
AGTCGCTATTTGATAAGCAAATAGCATATTTCTAAGTATTACCAAGTT  
ATTGTTATGGATAGTAGAGGGCATGGCAAAAGTCATGCAAAGCTAAATAC  
CATTAGTTCAAGCAAATAGCAGTTGACTAAAGGATATCTTAGTTCAATT  
35      AGAGATTGATAAAAGTTATATTGGTAGGCCATAGCGATGGTGCTAATTAGC  
TTTAGTTTCAAACGATGTTCCAGATATGGTTAGAGGGCTTTGCTTAAT  
TCAGGGAACCTGACTATTCAATGGTCAGCGATGGTGGGATATTCTTTAGTA  
AGGATTGCCTATAAATTCTTCACTATTAGGGAAACTCTTCCGTATATG  
AGGCAAAAAGCTCAAGTTATTCGCTTATGTTGGAGGATTGAAGATTAGT  
40      CCAGCTGATTACAGCATGTGTCAACTCCTGTAATGGTTGGTTGGAAAT  
AAGGACATAATTAAGTTAAATCATTCTAAGAAACTTGCTTCTTATTCCA  
AGGGGGAGTTTATTCTTAGTTGGCTTGGCATCACATTATTAAGCAA  
GATTCCCATGTTTAATATTGCAAAAAAGTTATCAACGATACTGTT  
AAAGGAGAAATTGTTGAAAAAGCTAATTGA

(SEQ ID NO: 36)

MTENWLHTKDGSDIYYRVVGQQPIVFLHGNSLSSRYFDKQIAYFSKYYQVIV  
5 MDSRGHGKSHAKLNTISFRQIAVDLKDLVHLEIDKVILVGHSDGANALVFQ  
TMFPDMVRGLLLNSGNLTIHGQRWWDILLVRIA YKFLHYLGKLFYMRQKA  
QVISLMLEDLKISPADLQHVSTPVMVLVGNKDIKLNHSKKLASYFPRGEFYSL  
VGFGHHIIKQDSHVFNIIAKKFINDTLKGEIVEKAN\*

10 Sequence description:

- A] Length: 744 bp - 248 aa (full length gene)
- B] No obvious signal peptide, but Shine Dalgarno sequence upstream of the ATG start codon.

15

ID-94

20 Clone RS-71

(SEQ ID NO: 37)

ATGGTAGCAAAAGAGTTAGGTAAAAATAGCTTACTATCCCAACTATTGT  
TCTAATTGCTCCGCAGGTACTGCCATTGCAGTTGTATATAATGATGACCAT  
25 TCTTCCTTAAGATACGGCTATCCCGAGTCTCCACTTCATATTTTATCAATA  
CACGGATCATTGCACAGGCACCAAGCAAATATTTTGGGCTGGTATTGGGG  
ACGGTATTCAAAAGCCCCTGAAGTAGAACGTGCTACCTTAGAGGCTAAG  
ACCAATAAAACTACCACATACTGCAGTGTAGGACAAGCAGTCGCTCTGTCT  
30 TCAAAGGAAGCTTTATCAATTGGTGAACAAGGTCTAAAGACGTTGAA  
GCTAATTAGCTCGCGTGCAGTTGAAGAAATTGCGCTTGATATCTTA

(SEQ ID NO: 38)

MVAKELGKNSFTIPTICSNCSAGTAIAVVYNDDHSFLRYGYPESPLHIFINTRIIA  
35 QAPSKYFWAGIGDGISKAPEVERATLEAKTNKLPTAVLGQAVALSSKEAFY  
QFGEQGLKDVEANLASRAVEEIALDIL

Sequence description:

40 A] Length: 405 bp - 135 aa (Partial sequence)  
B] No obvious Shine Dalgarno sequence upstream  
of the ATG start codon, probable signal  
peptide present at the N-terminus.

ID-95

Clone RS-73

5 (SEQ ID NO: 39)

TTGAGGGAAACTTACTGGAAAATTCAAGCGATTGCGATAAAATAATCTT  
GCAGAGTTTCTAGAGAAAGGAGGTCAGATTATTGGAGTGGCAAGATCT  
AGCGCAGTTACCTGTATCTATTAAAGACTATGTTACAGATGCTCAAGA  
CGCGGAAAAAACCTTTATATGGACAGAAGTATTAAAGGGAGATTAATCG  
10 CTCAAATCAAGAAATTATTGCATATTGGCCGATGACTAAGACAGTCAT  
TCTGGGGATGTTAGATCGAGAATTACCACATTAGAATTAGCTAAAAAAAG  
AAATCATCAGTCGTGGTTATGAACCAGTTGTTCGGAATTGGAGGTCTCG  
CAGTTGTAGCTGATGAAGGAATTAAATTTCATTGGTTATTCCAGATGT  
TTTGAGAGAAAATTGTCTATCTCAGATGGGTATCTTATAATGGTCGATT  
15 ATTAGAAGTATTTCGGATTTATCAACCTATTGAGCACTTGAAGTA  
GAGACCTCCTATTGTCCTGGTAAGTTGATCTTAGTATAAATGGCAAAAAAA  
TTTGCCTGGCTTGGCTCAGGCCGTATAAAGAATGGTATTGCGGTATCAATT  
TACCTTAGCGTTGTGGCGATCAAAAAGGGCGGAGTCAAATGATTTCAGAT  
20 TTTTATAAGATTGGTCTAGGTGATACGGGTAGTCCAATTGCTTATCCAAAT  
GTAGATCCTGAAATTATGGCTAATCTATCTGATCTATTAGATTGTCCTATG  
ACAGTAGAAGATGTTATTGATCGTATGTTGATTAGCCTAAACAAGTAGGT  
TTAATGATCGTTACTGATGATTAGACCCGATTAGTTGCAGAGTTGAT  
AGATTTCAGGCTAAGTCTATGGCTAATAAGGGATGGTGAGCAGAGATGA  
ATAA

25

(SEQ ID NO: 40)

MRETYWKISSDCDKINLAEFSRERRSDLLEWQDLAQLPVSIFKDYVTDAQDAE  
KPFIWTEVFLREINRSNQEIIHLIWPMKTIVLGMULDRELPHLEAKKEIISRGYE  
PVVRNFGLAVVADEGILNFSLVIPDVFERKLSISDGYLMVDFIRSIIFSDFYQPI  
30 EHFEVETSYPGKFDLSINGKKFAGLAQRRIKNGIAVSIYLSVCGDQKGRSQMI  
SDFYKIGLGDGTGSPIAYPNVDPEIMANLSDLLCPMTVEDVIDRMLISLKQVGF  
NDRLLMIRPDLVAEFDRFQAKSMANKGMVSRE\*

35

Sequence description:

40

A] Length: 921 bp -307 aa (Full-length gene sequence)

B] No obvious Shine Dalgarno sequence upstream  
of the TTG start codon or signal peptide  
visible. Actual start point may be a further  
85 bp downstream (TTG). This start point is  
preceded by a typical Shine-Dalgarno sequence.

ID-96

Clone RS-74

5

(SEQ ID NO: 41)

10

TTGGAAGGTTACTTATTGCATTGATTCCATGTTGCGTGGGAAAGTATT  
GGATTGTTAGTAATAAAAATTGGAGGGCGTCAAATCAACAAACATTGG  
AATGACTTAGGAGCATTGCTATTGCGATTATCGTATGGTTATTAAACA  
GCCAGAGATGACTGCCTCATTGTGGATTTGGTATCTTAGGTGGTATCCT  
ATGGTCAGTCGCCAAAATGGTCAATTCAAGCAATGAAATATATGGGAG  
TCTCTGTTGCTAATCCACTGTCAAGTGGTGCACAATTAGTAGGTGGAAGCC  
TAGTTGGTGCTTAGTCTTCATGAATGGACTAACCCAATTTATT  
AGGATTGACAGCGTTGACATTATTAGTTATCGGCTTCTATTCTCAAGTAA  
15

15

ACGTGATGTTCAGAACAGCTTGGCAACACATCAAGAGTTTCAAAAG  
GATTGCTACAATTGCTTATTCAACTGTAGGTTACATCTCGTACGCAGTTT  
ATTAAACAACATTATGAAGTTCGACGCTATGGCCGTCTTTACCCATGGC  
TGTTGGAATGTGCTAGGTGCAATTGTTCATGAAGTTCTGTGTTAACTTT  
GAGGCTGTTGTTAAAAATATGATTACAGGTCTCATGTGGGGCGTTGGT  
20

20

AATGTCTTCATGTTATTGGCAGCAGCTAAAGCAGGGCTAGCAATTGCTTT  
AGTTTTCTCAACTTGGAGTAATTATCTCTATTATTGGTGGTATTTTATT  
AGGTGAGACAAAACGAAGAAAGAGCAGAAATGGGTTGTATGGTAC  
CTTGTTGTTATGGGTCTATATTACTGGTATTGTTAAATCTTATTAA

25

(SEQ ID NO: 42)

30

MEGLLIALIPMFAWESIGFVSNKIGGRPNQQTFGMLGALLFAIVWLKQPEM  
TASLWIFGILGGILWSVGQNGQFQAMKYMGVSVANPLSSGAQLVGGSLVGAL  
VFHEWTKPIQFILGLTALTLLVIGFYFSSKRDVSEQALATHQEFSKGATIAYST  
VGYISYAVLFNNIMKFDAMAVALPMAVGMCLGAICFMKFRVNFEAVVVKNM  
TGLMWGVGNVFMLLAAAKAGLAIAFSFSQLGVIISIIGGILFLGETTKKEQK  
WVVMGILCFVMGAILLGIVKSY\*

Sequence description:

35

- A] Length: 867 bp - 289 aa (full-length gene)
- B] Possible Shine Dalgarno sequence upstream of  
GTG start codon, no obvious signal peptide  
present.

40

ID-97

Clone RS-75

(SEQ ID NO: 43)

ATGACAACTTACTACGAAGCTATAAACTGGAACGAAATTGAAGATGTTAT  
TGATAAAATCAACTTGGGAAAAACTAACCGAACAACTTGGCTCGATACAC  
5 GTATCCCTTATCAAATGACTTAGACGATTGGCGCAAACCTTCGCTCAAG  
AAAAAGATCTTGGCAAGGTTTGGAGGCTTAACCCTACTGATACCA  
TGCAATCAGAAACTGGTGTGAAGCTATTGTGCCGATGTCGCACGCCTC  
ACGAAGAAGCTGTCTAAACAATTCAATTGAAATCTGTTACGCTA  
AATCTTATTCTCAATTTCCTCAACTTAAATACTAAATCAGAAATTGAAG  
10 AAATTTCGAGTGGACTAATAATAATGAGTTCCCTCAAGAAAAAGCACGT  
ATTATCAATGACATTATGCTAATGGAAATGCCCTCAAAAAAAAGGTGGCT  
TCCACCTACCTCGAAACTTCCTTTATTCTGGCTTTCACACCTCTTA  
CTATTGGGAAATAATAAGTTAGCAAATGTTGCTGAAATCATTAAATTAAAT  
TATTGTGATGAATCTGTACATGGTACTTATATCGGTTACAAATTCCAGCTT  
15 GGTTTAACGAATTACCAAGAAGATGAGCAAGAGAATTTCGTGATTGGAT  
GTATGACCTCCTTATCAGCTGTATGAAAACGAAGAAAAATACACCAAGA  
CACTTATGATGGCGTAGGATGGACTGAAGAAGTTATGACCTTTACGCT  
ACAATGCTAATAAGCTTTATGAATTAGGACAAGATCCTTATTCCCAG  
ATACAGCAAATGATGTCAACCCATTGTTATGAATGGTATTCAACAGGAA  
20 CATCAAACCATGACTCTCTCAAGTAGGTAAATGGTACCTACTGGTA  
GCGTTGAAGCTATGCATGATGACTATAACTATGGATTATAA

(SEQ ID NO: 44)

MTTYYEAINWNEIEDVIDKSTWEKLTEQFWLDTRIPLSNDLDDWRKLSAQEK  
25 DLVGKVFGGLTLLDTMQSETGVEAIRADVRTPHEEAVLNNIQFMESVHAKSY  
SSIFSTLNKSEIEEIFEWTNNEFLQEKARIINDIYANGNALQKKVASTYLETF  
LFYSGFFTPLYYLGNKNLANVAEIJKLIIRDESVHGYIGYKFQLGFNELPEDEQ  
ENFRDWMDLLYQLYENEKYTKTLYDGVGWTEEVMTFLRYNANKALMNL  
30 GQDPLFPDTANDVNPIVMNGISTGTSNHDFFSQVGNGYLLGSVEAMHDDDYN  
YGL\*

Sequence description:

35 A] Length: 960 bp - 320 aa (full length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, but no signal peptide  
present.

40

ID-98

Clone RS-77 (partial sequence)

(SEQ ID NO: 45)

ATGAATTGGTCACGTATCTGGGAACCTCGTAAAAATTAATATCCTTATTCA  
AACCCTCAGACTCTATCGGCACTAAGAAAAAGCAAGAAAAGCATCCTAA  
5 AAAAGAATTTCAGCTATAAATCCATGTTAGAAATCAGTTATTCAGAT  
TTGCTCTTCAATAATTATGTATTCTCTTGATCACTGATTAAAG  
AATATCCGGGCTATTCACGTTCTACATTGGTATCTTACACTAGTATCCAT  
TATCTACTCTTTATTGCGATGTACAGTGTCTATGAGAGTGACGATGTT  
AA

10 (SEQ ID NO: 46)

MNWSRIWELVKINILYSNPQTLSALRKKQEKPKEFSAYKSMFRNQLFQILL  
FSIYVFLFVSLDFKEYPGYFTFYIGIFTLVSIYSFIAMYSVFYESDDV

15 Sequence description:

- A] Length: 311 bp - 103 aa (Partial sequence)
- B] Shine Dalgarno sequence present upstream of  
20 ATG start codon, no obvious signal peptide at  
N-terminus.

ID-99

25 Clone RS-78 (partial sequence)

(SEQ ID NO: 47)

TAATCTTTAGTCAACGGAGAACAGGAAAATTGCAGGCTATGCGACAGA  
TATTCCACCACATAATTAGCAGAAGTCATTGATGCTGTCGTACATGAT  
30 TGATCACCTAAAGCTAAATTAGATAAATTAAATGGAATTCTACCTGGTCC  
AGATTTCACACTGGCGCTATCATTCAAGGAAAAGATGAAATTGTAAGG  
CATATGAGACTGGTAAGGGAGAGTAGCGGTTCGCTCGCGAACTGCTATT  
GAAACCTTAAAGGTGGTAAGAAACAAATTATTGTTACTGAAATTCCCTAT  
GAAGTTAAT

35 (SEQ ID NO: 48)

SFSQRSNRKIAGYATDIPPHNLAEVIDAVVYMIDHPKAKLDKLMEFLPGPDFPT  
GAIIQGKDEIRKA YETGKGRVA VRSRTAIETLKGGKKQIIVTEIPYEVN

40 Sequence description:

- A] Length: 312 bp - 104 aa (Partial sequence)
- B] No obvious Shine Dalgarno sequence or a

signal peptide. Both N- and C- termini of ORF yet to be elucidated.

5 ID-100

Clone RS-79

(SEQ ID NO: 49)

10 ATGGGACGTAAGTGGGCCAATATTGTTGCCAAAAAGACTGCTAAAGATGG  
TGCTAACTCAAAAGTATACTGCTAAATTGGTGTGAAATATATGTTGCTGC  
AAAGCAAGGTGAACCAGACCCCGAGTCAAACTCAGCTCTAAAATTGTT  
TGGACCGTGCTAACAGCAAGCACAGTTCCAAAGCATGTTATTGATAAAGCG  
ATTGATAAAAGCCAAGGAAACACAGATGAAACTTCGTAGAGGGACGCTA  
15 TGAAGGTTTGGTCCAATGGTCAATGATTATTGTGGATACTTGACATC  
AAATGTTAACCGTACGGCAGCAAATGTACGTACTGCTTACGGTAAGAACG  
GTGGCAATATGGGAGCTTCAGGATCGGTATCCTACTTATTGATAAAAAAG  
GTGTCATCGTTTGCTGGTGTGATGCTGACACTGTCTCGAACAAATTACT  
TGAAGCGGATGTAGACGTAGATGATGTTGAAGCAGAACAGAGGGAACAAATA  
20 ACAGTTATACGCCCAACAGATCTTCATAAAGGTATCCAAGCACTTCGC  
GATAATGGTAGAAGAATTCCAAGTTACTGAACATTGATTCCCAA  
TCAGAAGTAGTATTGGAAGGTGATGACCTTGAAACTTTGAAAAGCTT

(SEQ ID NO: 50)

25 MGRKWANIVAKKTAKDGANSKVYAKFGVEIYVAAKQGEPDPESSALKFVL  
DRAKQAQVPKHVIDKAIDKAKGNTDETVEGRYEGFGPNNSMIIVDTLTSNV  
NRTAANVRTAYGKNGGNMGASGSVSYLFDKKGKVIVFAGDDADTVFEQLLEA  
DVDVDDVEAEEGTITVYTAPTDLHKGIQALRDNGVEEFQVTELEMIPQSEVVL  
EGDDLETFEKL

30

Sequence description:

35 A] Length: 654 bp - 218 aa (Partial sequence)  
B] Possible Shine Dalgarno sequence upstream  
of ATG start, no obvious signal peptide

40 ID-101

Clone RS-80

(SEQ ID NO: 51)

TTGGAGAAATATTGAAGAACCGATTACATGGATTGGATTAGTTCTTGTG  
GTTACGTGGTTTTAACTAAAAGTAGTGAATTGGATTGGTGTGTG  
TCTTGTGTTAGTATTGCTAGTCAAAGTGAT

5

(SEQ ID NO: 52)

MEKYLKNPITWIGLVLVVTWFLTKSSEFLIFGVCVLLLVFASQSD

10 Sequence description:

A] Length: 135 bp - 45 aa (partial sequence)

B] Shine Dalgarno sequence upstream of TTG

start codon with possible signal peptide

15 evident at N-terminus.

20 ID-102

Clone RS-81

(SEQ ID NO: 53)

ATGACACAATCAGATGCATATCTCTCGTTAACGCGAACACGCTT  
GATCGCACAGGTAATTATCATTACTTCGGATAAAGAGGGCTGTTAAC  
TATATGATAGAACATGTTAACCTAATACGATGGTGT  
CACATCACTAATT  
GAAAAGCTAGATTATTGGTTCTAATAACTACTATGAATCGGAC  
AAACAAATATAACCTTGAGTTATTGCCAAATTGGAGCATGC  
AAGAAAATTGCTTCTAAATTATGGGGCTTAAAATT  
30 ATGCTCTTAAT

(SEQ ID NO: 54)

MTQSAYLSLN  
AKTRFRDRTGNYHFTSDKEAVEQYMIEHVEPNTMVFTSLIE  
KLDYLVSN  
35 YYESDLLKQYNLEFICQIFEHAYAKKFAFLNFMGALKFYNAYA  
LN

Sequence description:

40

A] Length: 318 bp - 106 aa (Partial sequence)

B] Shine Dalgarno sequence present upstream of

ATG start codon, no obvious signal peptide

ID-103

Clone 2-11A

5 (SEQ ID NO: 55)  
ATGGTATTTATGGCAAATAAGAAAAAAACAAAAGGAAAGAAAAACCAGAA  
GACCTACTAAGGCAGAAATAGAGCGTCAAAGAGCTATTCAAAGGATGATT  
ACTGCTCTGTTAACATTATTCTCTTGGTATTATCAGATTAGGTA  
TTTTGGTATTACAGTCTATAACGTCACTCCGTTATGGTAGGTAGCTGGC  
10 TTACTTATTATTGCGGCAACTTAATCTACCTTATTCTTAAATGGTTG  
CGAAAGAAAGATAGCTTAGTAGCAGGTTTGATAGCTTCTTAGGATTA  
TTGATTGAGTGGCATGCTTACCTTCCTCAATGCCTATTGAAAGATAAA  
GAAATTTCGCTCAACTGCTCGATTAATTGTGTCTGATTAAATGCAATTAA  
AAATCACTGTTTGCCGGTGGAGGTATGTTGGTGCTTGATTACAAGC  
15 CAATTGCTTCTCTTAATATTGGTGCCTATATGATTGGTGTCTCTTC  
ATCATTGGGTCTCTTTAACATTGAGTTCTCTGGAAAGTTATGACATCGTCG  
AATTATTAGAGCTTTAAAAATAAAGTGGCAGAGAACGACGAGCAAAAT  
AAAAAGGAGCGTTGCTAACCGAGAGATGAAAAAGCAATCGCTGAACA  
AGAGCGCATAGAGCGTCAAAAAGCTGAAGAAGAACGTTATTAGCTTCGG  
20 TTAATGTAGACCCTGAAACGGGTGAGATTCTAGAGGATCAAGCTGAGGAC  
AATTGGATGATGCGCTACCACCTGAGGTAAGTGAAACATCAACTCCGGT  
ATTGAGCCAGAGATCCTGCTTATGAGACATCGCCTCAAAATGATCCTT  
ACCACTAGAGCCGACAATTATTAGAAGACTATGATTGCCGATTCTAA  
TATGAGAGAAAATGATGAGGAATGGTTATGATTAGATGATGATGTAG  
25 ATGATAGTGATATAGAAAATGTCGACTTTACACCTAAAACGACACTGGTT  
ATAAATTACCAACGATAGATTATTGCACCAAGATAAGCCTAAAAATCAAT  
CCAAAGAAAAGGATTAGTCCGAAAGAATATCAGAGTTAGAAGAAAACA  
TTAGAAGTTGGTATCGATGTAAAAGTAGAACGTGCTGAAATTGGACCA  
TCAGTTACTAAATATGAAATTAAACCAGCAGTTGGAGTCGTGAATCGT  
30 ATTCAAAATCTATGACGACCTAGCTCTGCTCTGCAGCAAAAGATGTG  
CGTATAGAACGACCAATTCTGGAAAATCATTAATAGGTATTGAAGTTCC  
AACTCAGAAATTGCAACGGTTCTTCCCGCAACTTGGGAACAATCTGAT  
GCCAATCCTGAAAACCTTTAGAAGTACCACTAGGAAAAGCTGTTAACGG  
CAATGCTCGCAGTTAACTTAGCTAGAATGCCGCATCTTGGTAGCTGG  
35 TTCAACTGGTTCAGGTAAATCTGTGGCAGTTAATGGAATTATTCAAGTAT  
TTTGATGAAGGCACGTCCAGATCAAGTTAAGTTATGATGATTGATCCC  
AAATGGTTGAATTATCTGTTATAATGATATTCCACATTATTAATCCCTGTT  
GTAACCAATCCCGTAAAGCAAGTAAGGCACCTCCAAAAAGTTGTTGATGA  
AATGGAAAATCGATACGAGTTATTAGCAAAATTGGTGTGCGTAATATAG  
40 CAGGTTATAATACAAAGGTTGAAGAGTTAATGCTCCTCTGAGAAAAAC  
AAATGCCTTGCCTTAATCGTTGTCATTGTAGATGAATTGGCTGACTTGAT  
GATGGTTGCTAGTAAAGAAGTTGAAGATGCTATTATTGCTTGGGGCAAAA  
AGCACGTGCTGCAGGTATCCATATGATTCTGCAACTCAACGTCCATCCGT  
AGATGTTATTCTGGTTGATTAAAGCAAATGTTCCGTCGCGTATTGCATT

GCTGTTCAAGTGGTACTGATAGCCGTACGATCCTGATGAAAATGGTGCT  
GAAAAGCTCTGGGACGGGGTGACATGCTCTTAAGCCTATTGATGAGAAT  
CATCCAGTACGACTACAAGGTTCTTATTCAGATGATGATGTTGAAAGG  
ATCGTTGGTTTATCAAAGACCAAGCCGAGGCTGACTATGATGATGCCTT  
5 GATCCTGGAGAAGTATCTGAAACAGATAACGGCTCTGGTGGTGGCGCGG  
AGTACCTGAAAGTGATCCTCTTTGAAGAACGCAAGGGACTCGTTAGA  
GACGCAAAAAGCAAGTGCCTCAATGATTCAACGCCATTGTCTGTTGGTT  
CAATAGAGCAACAAGACTAATGGAAGAATTAGAAGCAGCAGGGGGTTATTG  
10 GTCCAGCAGAAGGAACCAAGCCACGAAAAGTTTAATGACTCCAACCTCG  
AGTGAATAA

(SEQ ID NO: 56)

MVFMANKKKTKGKKTRRPTKAEIERQRAIQRMITALVLTIIFFGIIRLGIFGIT  
VYNVIRFMVGSLAYLFIAATLIYLYFFKWLRLKDSL VAGFLIASLGLLIEWHA  
15 YLFSMPILKDKIELRSTARLIVSDLMQFKITVFAGGGMLGALIYKPIAFLFSNIG  
AYMIGVLFIILGLFLMSSLEVYDIVEFIRAFKNKVAEKHEQNKKERFAKREMK  
KAIAEGERIERQKAEEEAYLASVNVDPETGEILEDQAEDNLDDALPPEVSETST  
PVFEPEILA YETSPQNDPLPVEPTIYLEDYDSPIPNMRENDEEMVYDLDDDVDD  
20 SDIENVDFTPKTLVYKLPTIDLFPAPDKPKNQSKEKDLVRKNIRVLEETFRSFGI  
DVKVERAEIGPSVTKYEIKPAVGVRVNRISNLSSDLALALA AKDVRIEAPIPGK  
SLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSFNLRMPH  
LLVAGSTGSGKSVAVNGISSLMKARPQVKFMMIDPKMVELSVYNDIPHLLI  
25 PVVTNPBKASKALQKVVDLEMENRYELFSKIGVRNIAGYNTKVEEFNASSEQK  
QMPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMLATQRPSVD  
VISGLIKANVPSRIAFAVSSGTDSTILDENGAEKLLRGDMLFKPIDENHPVRL  
QGSFISDDDVERIVGFIKDQAEADYDDAFDPGEVSETDNGSGGGGPESDPL  
FEEAKGLVLETQKASASMIQRRLSVGFNRATRLMEELEAAGVIGPAEGTKPRK  
VLMTPTPSE\*

30

Sequence description:

A] Length: 2451 bp - 817 aa (Full-length gene)

35

B] Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
peptide

ID-104

40

Clone 2-18/22b

(SEQ ID NO: 57)

ATGTCACAAGAGCAAGGAAAAATTATATTGTAGAAGATGATATGACGAT  
TGTGTCACTTTAAAAGATCATTATCAGCTAGCTATCATGTCTAGTGTC  
AGCAATTTCGTGATGTGAAACAAGAAATTATCGCATTCAACCCGATTG  
5 ATACTAATGGATATTACGTTACCCTATTAAATGGTTTACTGGACTGCAG  
AATTGCGTAAGTTTAACAATTCCATTATTCATTCATCTAGTAATGA  
TGAAATGGATATGGTTATGGCATTAAATATGGGGGGTATGACTTTATTG  
AAAACCATTCTCTAGCTGTATTAGATGCTAACGCTAACGCTATTAAAG  
10 GAGAAGTCAACAATTATCCAACAGGAATTAACTTTGGGGATTACGTT  
GACAAGAGAAGGGTATTGTCTAGCCAAGATAAAGAGGTTATTATCGC  
CAACAGAAAATAAAATCCTATCTATCTTGCTCATGCATCCTAAACAAGTAG  
TCTCAAAAGAGTCTCTATTAGAGAAACTTGGGAAAATGATAGTTATTG  
ATCAAAATACACTTAATGTTAATATGACACGCTTACGTAAAAAAATTGTCC  
20 CAATAGGTTTGATTACATTACAGTGAGAGGAGTTGGTATTACTAC  
AATGA

15 (SEQ ID NO: 58)  
MSQEQQKIVIVEDDMTIVSLLKDHL SASYHVSSVS NFRDV KQEI IA FQPDLILM  
DITLPYFNGFYWT AELRKFL TIPIFI SSNDEM DMV M ALNM GGDD FISK PFSLA  
VLD AKL TAIL RRS QQF IQQL TF GGFT LTRE GLL SS QDKE VILS PTEN KIL SILLM  
HPK QV VS KES LLE KL WEND SFID QNT LN VN MTRL RKK IVP IGF DYI HT VRGV G  
25 YLLQ\*

Sequence description:

25 A] Length: 669 bp - 223 aa (full-length gene sequence)  
B] Shine Dalgarno sequence present upstream of a GTG start codon.  
Was not identified directly by LEEP. This gene was found upstream of  
30 gene ID-10 described in WO 00/06736.

ID-105

35 Clone 2-20

(SEQ ID NO: 59)

40 ATGTATCAA ACTCAGACAA ATAAGGAAAA ATTGTTT ATTGAA ATT  
TTTATCCCAGTATTGATTATCAATTGCTAATTTCAGCTACTTTATTGA  
TTCGGTTATGACTGGACAGTATAGTCAGCTACATTGGCAGGTGTCAAC  
TGCTAGTAATTATGGACTCCGTTTCGCTTATTAGTAGGTATGATTCA  
GCATTAGTACCA CAGTAGTTGGTCAACATTGGTAGAGGAAATAAGAAC  
AATT CGCACAGAATT CATCAATTCTATATTAGGTTGATACTGTCCTTA  
ATATTATTTAATCATGCAATTATTGCTCAACCTGTCTGGGGAGTTGG

5 GTTTAGAAGATGAAGTTCTAGCAGTTGGCGTGGTTATTAAATTATATGT  
TGATTGGAATCATGCCGCTGGTGTAGCATTGCCGTCATTCTTGA  
TGCATTGGGGTTAACAAAGGTATCTATGTATCTGATGCTTTAATTCTACCC  
TTAATTCACTTTAATTATGCTTATCTACGGTAAATTGGTATGCCTA  
10 GACTAGGAGGTGCGGGGCAGGTCTTGGAACTTCTTAACCTATTGGGCTA  
TTTTATTGGTATTATTGTGATGTCACTCATCCTCAAATTAAAACATA  
TCATATATGGACTCTGGAAAGAATAAAAGCTCCTTGATTATTGAAGATAT  
TCGATTGGGATTACCGATTGGTTACAAATTTCAGAAGTTGCAATT  
15 GCAGTAGTAGGCTTATTCACTGGAAAATTCTCAATCATTATTGCAGCA  
CATCAGGCTGCTATGAATTTCATCATTAAATGTATGCATTCTTAAGTA  
TTTCCACTGCTCTAGCTATTACAATATCGTTGAAGTAGGGCAGAGCGCT  
TTCAGGACGCAACCACCTATAGTAGGATAGGACGCTAACAGCGGTAGGG  
ATTACATCAGGAACCTTACTATTATTCTATTCTGAGAATGTAGCAG  
20 CAATGTATAATAGTCCCCCTCACTTGTGCTATTACAGCTCAATTCTAAC  
TTATAGTCTCTTTCCAGTTGCAGATGCTTATGCAGCTCCTGTACAGGGG  
ATTACGAGGCTATAAGGATACAACAAAACCATTATGATCGGTGCGGG  
CTCTTATTGGTTATGTGCTTGCCTATTGGATTGGTTAACACAGGTATT  
CCAGTTAGGTCCGTTGCCTATTGGATTGGTTAACACAGGTATT  
TGTGGTCTATTCTAACCAACGTCTGCAAAAGATTAAGAAGTTGTATTAT  
TAA

(SEQ ID NO: 60)

25 MYQTQTNKEKFVLFLKLFIPVLIYQFANFSATFIDSVMTGQYSQLHLAGVSTAS  
NLWTPFFALLVGMISALVPVVGQHLGRGNKEQIRTEFHQFLYLGLLILSLILFLI  
MQFIAQPVLGSLGLEDEVLAVERGYLNMLIGIMPLVLFSCRSFFDALGLTRL  
SMYLMLLILPFNSFFNYMLIYGKFGMPRLGGAGAGLGTSLTYWAIFIGIIIVMS  
LHPQIKTYHIWTLERIKAPLIIEDIRLGLPIGLQIFAEVAIFAVVGLFMAKFSSIIA  
30 AHQAAMNFSSLMYAFPLSISTALAITISFEVGAERFQDATTYSRIGRLTAVGITS  
GTLLFLFLFRENVAAMYNSAPHVAITAQFLTYSLFFQFADAYAAPVQGILRG  
YKDTTKPFMIGAGSYWLICALPLAVILEKNSQLGPFAYWIGLITGIFVCGLFLNQ  
RLQKIKKLYY\*

35 Sequence description:

- A] Length: 1341 bp - 447 aa (full length gene)  
B] Shine-Dalgarno sequence present upstream of  
ATG start codon, There is a potential signal  
peptide sequence

40

ID-106

Clone 2-4A

(SEQ ID NO: 61)

5 TTGCTAGTTCTTCTAGTTCTGTCATTTCTGTCATTCTCGTCGTT  
CTTATTATCAATTTCATAAAATGCTATAATAAAAACCATGTCATTCA  
TTAAAAATTAGAAATCCATACGGTGAACATACCGTTAAAGAACCTCCTGA  
AGATTATTTTGATTCCACGTAAGAGATTAGACATTGGCTGTAAAAAAA  
10 CATGTACTTATAAACAAATGAATTCAATTGGCAAACGTGTCAGAA  
AACGATACTATTACCTTAATCTTGATGATGAGGATTACCTACTAAAAAAA  
ATTCCCTCTGGGCAGAGCAGAGCTATTGATTGTCTTATGAGGATGAACAT  
CTTATTATCGTTAATAAACCTGAAGGTATGAAAACTCACGGTAACCAACCA  
AATGAAATAGCACTGTTAAATCATGTATCTGCCTATTCTGGACAAACATGC  
TATGTTGTTCATCGCCTAGATATGGAGACCAGTGGAGCTGTTTATTGCT  
15 AAAAATCCATTATACTTCCCCTTATCAATCAACGCTTAGAACGAAAAGAA  
ATTGGCGTGAATATTGGGCTTAGTTGAAGGAAAATTTCACCTAACGAT  
CAAGTTTGAGAGACAAAATTGGACGGAACCGTCATGACAGACGTAACACG  
AATCATTGATTCTAAAAACGGTCAACATGCTATGACAATCATTGACGTTT  
GAAGTATATCCAAAATAGTAGTCTCATAAAATGCCGACTGGAAACCGGAA  
20 GAACCCATCAAATTGCATTCACTTATCTCATCACGGACATCCTTAATAG  
GAGATCCCCTCTACAACCCCTTCTTAATAATGAAAGGTTAATGCTACACG  
CTCACCGATTGACTCTATCCCATTAACTGCGAAACTATTAGCGTAG  
AGGCCCTTCATCTACTTCGAGAAGGTTTAAACAATTATAAAAAGGAG  
TTGGATAA

25

(SEQ ID NO: 62)

MLVSSLVSCSFFLVISSLSSSTRNKSINLSNNFIDLLYQFSIKCYNKTMFSLKIR  
NPYGEHTVKELLEDYFLIPRKIRHFLRVKKHVLINNEFINWQTVVQENDTITLIF  
30 DDEDYPTKKIPLGRAELIDCLYEDEHLIIVNKPEGMKTHGNQPNEIALLNVSA  
YSGQTCYVVHRLDMETSGAVLFAKNPFLPLINQRLERKEIWREYWALVEGKF  
SPKHQVLRDKIGRNRHRRKRIIDSNGQHAMTIIDVLKYIQNSSLIKCRLETG  
RTHQIRIHLHHGHPLIGDPLYNPSSNNERLMLHAHRLTLSHPLTCETISVEAPS  
STFEKVLNNYKKGVG\*

35

Sequence description:

40

- A] Length: 1029 bp - 343 aa (Full length gene sequence)
- B] No obvious Shine-Dalgarno sequence upstream  
of the putative TTG start codon. Possesses a  
potential leader peptide sequence.

ID-107

Clone 2-54

5 (SEQ ID NO: 63)  
GAACTAAATGCAACTCAACCTAATAATAGAACTACCTATATTATAACCGAA  
AGCAGTCATTCCATTGCAGAACACAACAGAGATTCTGATAGAATCAAAGGG  
TTCTTCGGTTGCATTACTTAATAGCGATGAATTAGAAAGACAGCAGGGAGA  
GGATAGAGGTTTGAAAGGGATAAGTTGAGGTCTTGGATATCATTCTAA  
10 GGGAGATTATCGACAAGTAATGTCATAGGTAATACGGACATTGCTAGTC  
AGATATCGTTGGGCTTAAAAAGAATGCGATGCAGGAACACCATCTTACT  
AAAACATTCTCTCAAAAGGATGGAAAGTTATCGTCTGTTATAGAGGGGAT  
GCTTGCTATTGGCAAAGAGAAAAGTAGAGAGAAAGAAAATAATAGGGTA  
ATTATGGCAAAAATTAAAAGCTAAGGCACACTGCCCTGTTGCTGTGTTG  
15 ATAATTGAATTGAAAGATATAAAATCTTATTTCATATTATTGTCATCT  
AAACCATCAGCTCAAATTACCTAAAGGTGCTATACTTCTGCTAAAACAGA  
AGTATATAGGGGAGGAGATTGGGAGAAAAAAATAAGATAATGTGTTG  
GTTACCGTATCCCCTCATTATTGAAAACCCAAAAAGGAACTTACTGCGG  
GAGCTGATGAAAGAATTGAGCAAGCTTGTGATTGGGAAACATAGGAATG  
20 GTTATTGCCGTAGTGAGGATGATGGTGTCACTTGGGAAAAAGAGAAC  
TATTGTCAATCTCCGTAAATAACCCTAGAGTTCCGCTAGTTACTAGTGGTGA  
CTATAGTGGCTCACCTATTAATATGGATATGGCATTAGTTCAAGATACTAG  
CTCCAAGACGAAACGTATTTTCAATATATGATATGTTCCAGAAGGAAG  
AGGCGTTATTAGTATTGCTAACACACCTGAAAAAGAATATAACCAAATCG  
25 GAGGACAGTCTTATCTAATTATAATAATGGAAAGAAATCGAAGGTTT  
TTACTATCCGTGACAAAGGTATTGTATATAATTAAAGGGAAAAAGACTG  
ATTATCATGTTATAACAGAAACTACTAAAAGTGACCATTCAAATCTAGGGG  
ATATTATAAGGGAAAACAGCTACTTGGAAATATATATTACAAAACATA  
AAACGTCACCATTGTTAGCAAAATCAAGCTATGTGTGGATGTCAATATA  
30 GCGATGATGATGGTAGGACATGGTCATCACCTAGAGATATAACAGCAAGT  
CTTCGTCAGAAAGGCATGAAATTGGGAAATAGGACCTGGAAAAGGTAT  
AGTTTAAAATGGGGCCACACGCTGGTGTATTATTATTCTGCCTATTCT  
ACGAATTGGAAATCTCATCTAAGAGGTTACAATCTCACGCCTAATTAT  
TCAGACGACCATTGGAAAAACGTGGCATACTGGAAAAGCAGTTAATGATAA  
35 CCGTATACTTCTAATGGTAAAAAAATTCACTCCTAACAAATGGATAATAA  
AAAAGAACAAAATACAGAACCGTACCCGTTCAATTGAAAATGGGGACA  
TTAAGTTATTATGAGGAATCTAACTGGTAACCTAGAAGTAGCCACAAGTA  
AAGACGGGGAGACTTGGCAAAACCATGTTAACACGATATAAGGAAATT  
CATGATGCTTACGTCCAACATCAGCTATTGCTTGTGAGCATGACAAAAAA  
40 GAGTATATTATTAGTGAATGCTAATGGGCCAGGGAAAGAAGTGCCAAGA  
TGGATATGCACGTCTAGCGCAAGTTAACGAAATGGTAGTTAAGTGGTT  
ATATCACCACATTCAAGATGGTCCTTACAACCTGTTCAACAA  
ACTTAATAATGATCAATTGGTGTCTTATGAACATAGAGAAAACATCA  
AAATAGTTACTTAAATTACAAAGTTTAATTGGAGTTCTTAGTCAA

AATACAGAGAAGCAAGGCACTTATGGGAGAAAATGGCAGCAAATTGGCA  
TGTGTTAAATTATTAATG

(SEQ ID NO: 64)  
5 ELNATQPNNRTTYIIPESSHSIAEQQRFLIESKGSSVALLNSDEFRKTAGEDRGF  
ERDKLRSLDIIPKGDLSTSNVIGNTDIASQISLGFKKNAMQEHHLTKTFSQKD  
KLSSVIEGMLAIGKEKVEKEIKYSGNLWQKLAKAHCLVCCVDNLNFEDIKS  
YFQYYCHLNHQLKLPKGAILSAKTEVYRGDFGRKNKDNVFGYRIPSLLKTQ  
10 KGTLLAGADERIEQACDWGNIGMVRSEDDGVTWGKRETIVNLRNNPRVPL  
VTSGDYSGSPINMDMALVQDTSSKTKRIFSIYDMFPEGRGVISANTPEKEYTQI  
GGQS YLNLYNNNGKKSKVFTIRDKGIVYNFKGKKTDYHVITETTKSDHSNLGDI  
YKGKQLLGNIYFTKHKTSPFRLAKSSYVWMSYSDDDGRTWSSPRDITASLRQ  
15 KGMKFLGIGPGKGIVLKWGPHAGRIIIPAYSTNWKSHLRGSQSSRLIYSDDHG  
KTWHTGKAVNDNRILSNGEKIHSLTMDNKKEQNTESVPVQLKNGDIKLFMRN  
LTGNLEVATSKDGGETWQNHVKRYKEIHADYVQLSAIRFEHDKEYILLVNA  
NGPGKKCQDGYARLAQVNNGSFKWLYHHHIQDGSFAYNSVQQLNNDQFG  
VLYEHREKHQNSFTLNYKVFNWSFLSQNTEKQGTLWEKMAANWHVLFKFYL  
\*

20 Sequence description:

- A] Length: 2052 bp - 684 aa (partial gene sequence)
- B] N-terminus has yet to be determined

25 ID-108

Clone 2-61

30 (SEQ ID NO: 65)  
ATGCCTAAATTAAATCGTATCTTCCTCTGCATTTATTATCCCTGACTTGTG  
TAAACTCTGTGCAAGCTGAAGAACATAAAGATATTATGCAAATTACCGA  
GAAGCCGGATATGATGTTAAAGATATTAAATAAACCTAAAGCGTCTATCGTT  
35 ATTGACAATAAAGGTCATATTTGTGGGAAGATAACGCCGATTAGAACGT  
GATCCCGCTAGCATGTCTAAAATGTTACTTATATTACTATTGAAGACT  
TAGCTAAAGGAAAAACAAACCTCAACACCACAGTGACTGCAACAGAAACA  
GACCAAGCCATAAGTAAGATTATGAAATTAGTAATAACAATATTGATGCT  
GGGTTGCTTATCCTATTGTAACGTGATTACTATGACGGCTGTCCCGTCA  
TCTAATGTAGCAACTATTATGATTGCTAACCACTTATCACAAAACAATGCT  
40 GACGCCTTATTAAACGAATCAATGAAACCGCCAAGAAACTCGGTATGAC  
AAAAACTCACTTTATAACCCCAGTGGGGCGGTAGCGAGTGCTTTAATGG  
ACTTTACTCCCCAAAAGAATACGATAACAATGCTACTAACGTTACGACTGC  
ACGTGATCTATCAATTAAACCTATCATTCCCTAAAAAATACCCGTATATA  
CTGAACATACAAAATACCTGAAGTCAAGGCCATGGTCGGAACCTCCTAT

GAAGAACATTACAACCTATAACTACTCTACCCCCGGCGCTAAATTGGA  
TTAGAAGGAGTAGATGGCTAAAAACTGGTTCTAGCCCTAGCGCTGCTTT  
AATGCCTTAGTTACAGCTAAACGCCAGAATACTCGCTTGATAACTGTGGTT  
5 TAGGAGTTGGCGATTGGTCAGACCAAGACGGAGAGTACTATCGTCATCC  
GTTTGTCAACGCTCTTGTAGAAAAAGGTTTAAAGACGCTAAAAATATTTC  
TTCTAAAACCTCCTGTATTAAAAGCCGTTAACCTAAAAAAGAAGTTACTAA  
AACCAAAACTAAATCTATTCAAGAACAGCCTCAAACAAAAGAACAGTGGT  
GGACAAAAAACAGATCAATTATCCAATCACATTGTATCTATTAAATTG  
10 TTCTGGGCACCATCGCTAGCCTTGTCTTAGCTGGATAGTATTACTTAA  
AAAGCGCTCTAGATAA

(SEQ ID NO: 66)  
MPKLIVSFLCILLSLTCVNSVQAEHKDIMQITREAGYDVKDINKPKASIVIDN  
KGHILWEDNADLERDPASMSKMFYLFFEDLAKGKTNLNTVTATETDQAI  
15 SKIYEISNNNIHAGVAYPIRELITMTAVPSSNVATIMIANHLSQNNPDAFIKRINE  
TAKKLGMTKTHFYNPSGAVASAFAFNGLYSPKEYDNNATNVTTARDLSILTYHF  
LKKYPDILNYTKYPEVKAMVGTPYEETFTTNYSTPGAKFGLEGVDGLKTGS  
SPSAAFNALVTAKRQNTRLITVVLGVGDWSDQDGEYYRHPFVNALVEKGFK  
DAKNISSKTPVLKAVKPKKEVTKTKTTSIQEQPQTKEQWWTKTDQFIQSHFVS  
20 ILIVLGTIASLCLLAGIVLLIKRSR\*

Sequence description:

25 A] Length: 1188 bp - 396 aa (full length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
peptide

30

ID-109

Clone 45

35 (SEQ ID NO: 67)  
ATGACTGAAAAATTATAATTGGCAACGCTTGGAACCGGCGTTATTGCC  
AACGAATTAGCCAAGCACTGGAAGCACGTGGACAAAAATTATATTCTGT  
AGCTAATAGAACTTACGACAAAGGACTTGAATTGCTAACAAATATGGTA  
TCCAAAAAGTTATGATCACATAGATCAAGTATTGAAGAACCTGAAGTGG  
40 ATATCATTATATCTCTACTCCCCACAATACTCACATCTCATTACGAAA  
GGCTTAGCAAATGGTAAGCACGTTCTTGCAGAAAAATCTATTACTTTAAA  
TAGTACTGAGCTAAAGAACCATAGATTTAGCCAAACTAACCATGTTGT  
CTTAGCTGAAGCCATGACTATTTCATATGCCAATTACCGCCAATTAAA  
AACATTAGTTGATAGGGAAAATTAGGACCGTTAAAAATGATTCAAATGA

ATTCGGAAGTTATAAAGAACATGATATGACTAACCGTTTCAGTCGTG  
ACCTAGCAGGCGGTGCCTTGCTGGACATTGGTGTATGCACTTCTTGTAT  
TCGCTGGTTATGTCAGAACGACCTCACAAACATTACCTCTCAAGTTACATT  
5 TGCACCAACAGGGGTTGATGAACAAGTTGGTATCCTACTAACCAACCCAG  
CAAATGAGATGGCGACTGTCAGCCTAGTTACATGCAAAACAAACCTAAA  
CGAGCAACTATCGCTTACGATAAAGGCTACATTGAACCTTTGAATATCCG  
CGAGGACAAAAGGCAGTTACTTACTGAGGATGGGCATCAAGATAT  
TATCGAAGCTGGCAAAACTGAAAATGCTCTCCAATATGAGGTAGCTGATA  
10 TGGAAGAACCCATTTCAGGAAAAACTAACACATGTACTTAAACTATACC  
AAAGATGTTATGGATATCATGACACAGCTACGTCAAGAACGGGATTAC  
CTACCCAGAAGAAGAAAAATGA

(SEQ ID NO: 68)

MTEKYYNWATLGTGVIANELAQALEARGQKLYSVANRTYDKGLEFANKYGI  
15 QKVYDHIDQVFEDPEVDIYISTPHNTHISFLRKALANGKHVLCEKSITLNTEL  
KEAIDLAEVNVLAEAMTIFHMPYRQLKTLVDSGKLGPLKMIQMNFGSYK  
EYDMTNRFFSRDLAGGALLDIGVYALSCIRWFMSEAPHNITSQVTFAPTGVDE  
QVGILLTNPANEMATVSLSLHAKQPKRATIAYDKGYIELFEYPRGQKAVITYT  
20 EDGHQDIIEAGKTENALQYEVADMEEAISGKTNHMYLNYTKDVMMDIMTQLR  
QEWGFTYPEEEK\*

Sequence description:

25 A] Length: 984 bp - 328 aa (full length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
peptide

30 ID-110

Clone 2-2

35 (SEQ ID NO: 69)  
GTGTATTCTCCTGTTAAATCTTCTAAAGGAAAAGTGATATTGTTAAAAAGT  
GATTTCTAAAGAGCTTCATAGAAAGGAGAGGAAATATTGTTTT

40 (SEQ ID NO: 70)  
MYSPVKSSKGKVILLKSDFLKSFERRGNICF

Sequence description:



A] Length: 96 bp - 32 aa (partial sequence)  
B] GTG start codon - no obvious Shine-Dalgarno  
sequence  
Possesses a potential signal peptide

5

ID-111

Clone 2-3

10

(SEQ ID NO: 71)

AAATACTGTATCATTGCAACCTCAAATGCAGGTTGGAAACGAAGCATT  
ACAGGTGACAGCGATAAAAGACTGAAAATTATGGAACGAATTCTCCATA  
TTTCCGTCCAGAATTCTAAATCGTTCAATGGTGTATTGAATTCTCTCAC  
15 CTAAGCAAAGATGACTTAAGCGAAATTGTAGATTGATGCTTGATGAAGTT  
AACCAAAACAATTGGCAAAAAAGGAATTGACCTTGTGGTAGATGAAAATGT  
TAAATCACACTTAATTGAACCTGGTTATGACGAAGCAATGGGAGTACGTC  
CATTGCGCCGTGTCATCGAGCAAGAAATTGAGATCGCATCACAGACTACT  
20 ATCTCGATCATACAGACGTTAACACCTAAAAGCTAATTGCAAGATGGCC  
AAATCGTCATTCTGAAAGATAA

(SEQ ID NO: 72)

KYCIIATSNAFGNEAFTGDSDKDLKIMERISPYFRPEFLNRNGVIEFSHLSKD  
DLSEIVDMLDEVNQTIGKKGIDLVVENVKSHLIELGYDEAMGVRPLRRVIE  
25 QEIRDRITDYYLDHTDVKHLKANLQDGQIVISER\*

Sequence description:

30

A] Length: 429 bp - 143 aa (partial sequence)  
B] N-terminus yet to be elucidated. This gene  
was not in frame with nuc

35

ID-112

Clone 2-5

(SEQ ID NO: 73)

40

ATGTCAATGAATTTTCATTTTACCAACATATTGGTCCTATTTAATTATG  
GTGTGATGGTAACCATTATGATTCAACATGTGTTTTGGAACTAT  
TATAGGCGTGTAAATTGCTTAGTAAAGCGTACTAATTACATTTCTCACA  
ATATTAGCTAATTCTATGTATGGGTATTCGTGGGACACCGATGGTAGTT  
CAAATTATGATTGCTTCGCATGGATGCATTTAACAAATTACCAACAATT

AGCTTTGGTGTAGATTACGACTTACCTGGTATCATT  
TCATTCCTAAATAGTGGTGCCTATATTCGGAAATTGTACGTGCAGGGA  
TTGAGGCTGTACCATCTGGACAAATAGAAGCAGCTACTCGTGGGGATT  
5 GACCTAAAAATACACTTCGCTATGTTCTTACCCCAAGCTTTAAAATA  
TTTACCTGCTCTAGGGAATGAATTATTACAATTATTAAAGATAGTGCTCT  
CCTTCAAACATTGGTGTACGGATTATGGAACGGAGCACAACTCAGTTGT  
AACGGCTACTTACTCACCAGTTGCACCGTTATTATTGCAGCATTACTAT  
TTAATGTTGACAACGATTCTCTCAGCTTGTAAAACAAATGGAGAAATAT  
CTTGGGAAAGGGTAAAAATAGATGGTTGA

10

(SEQ ID NO: 74)

MSMNFSFLPQYWNSYFNYGVMVTIMISTCVVFFGTIIGVLIALVKRTNLHFLTIL  
ANFYVVVFRRGTPMVVQIMIAFAWMHFNNLPTISFGVLDLDFTRLLPGIIIISLN  
15 GA YISEIVRAGIEAVPSGQIEAA YSLGIRPKNRLRYVILPQAFKNILPALGNEFITI  
IKDSALLQTIGVMELWNGAQSVVTATYSPVAPLLFAAFYYLMLTTILSALLKQ  
MEKYLKGKVIDG\*

Sequence description:

20

- A] Length: 699 bp - 233 aa (full length gene)
- B] Shine-Dalgarno sequence preceded the 'ATG' start codon. Possesses a potential leader peptide sequence.

25

ID-113

Clone 2-7

30

(SEQ ID NO: 75)

ATGAAAGACCTATTACGAAATAGCTAGAGCAAAGTGGAAATTAAAGTT  
TCAAGATATGATTTACATATTCTGTAGCAGCTTATTGAGTGTAGTTATT  
TATGTTCTATGCTTACGCATAGTGGAACTGCCTATAGTAAAAGTT  
35 AATGTTCATTAATGACATTGACGGTCTGACTGCAACAGTAATGACCGTT  
ATTGGTAATAATGTAGCCTGTCATTGGGTATGGTCGGTGCCTGTCAGTT  
GTTCGTTTAGGACAGCCATAAAAGATTCAAGAGATACTGTTATATT  
TGGACCATAGTTGTTGGTATCTGTTGTTGACTATGTGGTAGCT  
GCATTAGGAAGTAGCGTTATCTTATCTTATTATGGGTTATGGGACGTGTT  
40 AAAAACGAGAATCGTATGTTATTGATTGTGAAGTGCATAGAACACTAGA  
AGTTGATTAGAAGGAATTCTTCCAATATTGACGGAAAAGCTGTTCA  
GCGTGTAAAAATTCAACAACTAATACTATTGAAATGATTCGAAATCTC  
TAGAAAAGATTACGATAAGCAACTCCATGTAGATAATCAGTTAACTGAAA

AAGTGTACCAATTGGGAAATATTGATTATTCAACATTGTTAGCCAAAGCG  
ACGAAATCAATGGGTAG

(SEQ ID NO: 76)

5 MKDLLRNSLEQSGNLSFQDMILHILVAALLSVVIYVSYAYTHSGTAYSKKFNV  
SLMLTLVLTATVMTVIGNNVALSLGMVGALSVVRFTAICDSRDTVYIFWTIV  
VGICCGVGDYVVAALGSSVIFILLWVMGRVKNENRMLLIVKCDRTLEVLEGI  
FFQYFDGKAVQRVKNSTNTIEMIFEISRKDYDKQLHVNDNLTEKVYQLGNID  
YFNIVSQSDEING\*

10

Sequence description:

A] Length: 678 bp - 226 aa (full-length gene)

15 B] ATG start codon is preceded by a Shine-  
Dalgarno sequence-Possesses a potential leader  
peptide sequence

20 ID-114

Clone 2-8

(SEQ ID NO: 77)

25 AAAAATTCACTTCTAGATTCTTACGACTATATACTCAGAAGTACCAAAC  
CTAACCCAAGGTTGAAAAAAAGAAAGAAGGAAGTCAGTATGACAAACTAT  
AAAAACAACTTAAAGATGAGGCTATACGTGTTGAAGAGAGACAACAAAAGA  
ATCATTTCACGATGTTGATATTGCCTTGTTCAGCTGGTGGATCTATTCA  
GCAAAGTTCGCTCCTTATGCAGTAAAGTCTGGAGCAGTTGTTAGATAAC  
30 ACGTCATATTTCGTCAGAACCTTGATGTTCCACTAGTTGTTCTGAAGTAA  
ATGCTCATGCCATGATTGGTCATAATGGTATCATAGCTTGTCCCATTGTTG  
TACTATTCAAATGATGATTGCTTAGAGGCCATTGTCAAAAATGGGGGAT  
AGAGCGTGTATAGTTCCACCTATCAAGCTGTTGGGTTCAGGTGCACG  
TGCTGTTGAAGAACTAAGGAACAGTTGAGACAAAGTTT

35

(SEQ ID NO: 78)

KFILDSFYDYILRSTKPNSPRFEKRKEVSMTNYKNNFKDEAIRVEETTKESFYD  
VDIALFSAGGSISAKFAPYAVKSGAVVVDNTSYFRQNPDVPLVVPEVNAHAMI  
GHNGIIACPNCSTIQMMIALEPIRKWGIERVIVSTYQAVSGSGARAVEETKEQ  
40 LRQV

Sequence description:

A] Length: 499 bp - 165 aa (partial sequence)  
B] N-terminus has yet to be determined

5 ID-115

Clone 2-9

(SEQ ID NO: 79)

10 ATGACAAATGAATTGATAATGCAAGCTTTGAGTGGTATTACCTAGTGAT  
GGGAATCACTGGAAGAAATTAGAGGAGTCTATATCAGACCTTAAAAAAACT  
TGGAATTAGTAAAATCTGGTTACCACCAGCATTAAAGGAACTAGCAGTG  
ATGATGTAGGATATGGTGTATGATCTCTTGATTAGGAGAATTGACC  
AGAATGGAACAATTAGAACAAAATATGGTAGGAAAGAAGAGTATCTAAA  
15 GCTTATTAAGTCGTTAAAGGCAAATGGCATTAAACCGTTGCAGATATCGT  
TCTTAACCATAAAGCCAATGGTGATCATAAAGAAAAATTCAAGTCATCA  
AAGTCAATCCTGAAAATCGTCAAGAACGATTAAAGTGAACCCATTGAGATT  
GAAGGATGGACGGGATTGATTCCCAGGTAGACAGGGTGAGTACAATGA  
TTTT

20

(SEQ ID NO: 80)

MTNELIMQAFEWYLPSDLGNHWKKLEESISDLKLGISKIWLPPAFKGTSDDV  
GYGVYDLFDLGEFDQNGTIRTKYGRKEEYLKLKANGIKPFADIVLNHKA  
NGDHKEKFQVIKVNPENRQEALSEPYIEGWTGFDFPGRQGEYNDF

25

Sequence description:

A] Length: 456 bp - 152 aa (partial sequence)

30

B] ATG start codon is preceded by a Shine-Dalgarno sequence, no leader peptide sequence.

35 ID-116

Clone 2-10

(SEQ ID NO: 81)

40 ATGGAGGTTCTTATGAAGAAAGTGTAGTAAGTAGTCTTTGGTTTAGGG  
ATTACGATAACGTTACAACCAAGTAGTTGAGGCTAAGGGGCCAAAAGTAGC  
TTATACACAAGAGGGAATGACTGCTTTGGACACAAATAAGATAAAAG  
TCACTACTATTCTATTGACGAGATTCAAAAAAGCTAGAAGGTAAGAAGC  
CGATTACTGTTAGTTGATATTGATGATACTGCTTTCACTAGTCATAA

5 TTTCAATATGGTAAAGAATATGTAACCTCCTGGATCGTTGATTTCTTCAT  
AAACAAAAATTCTGGGATCTTGTGCAAAACGAGGAGATCAAGATTCCAT  
TCCCAGAATATGCTAAAAATTAAATTGCTATGCATCAAAACGAGGAG  
ATAAAATTGTTTATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAG  
GGCGAGGTTGATAAAACAGCTAAAGCCTAGCTAAAGATTAAATTGTA  
CCATCTGAT

(SEQ ID NO: 82)

MEVLMKKVLVSSLLVLGITITLQPVVEAKGPVAYTQEGMTALSDTNKDKVT  
10 TISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQYGKEYVTPGSFDFLHKQKF  
DLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGSMYKEGEVDKTA  
KALAKDFKFVPSD

15 Sequence description:

A] Length: 516 bp - 172 aa (partial sequence)

B] ATG start codon is preceded by a Shine-Dalgarno sequence, Possesses a leader peptide sequence.

20

ID-117

25 Clone 2-17

(SEQ ID NO: 83)

ATGCTAAAAGATTATTTACTGAAGATGGGAATTGACAAAGATTAGTCGT  
CGTTTCGTTGGATGTTAGTGGTTATCTATTGTCTTATTATTGTCAGGATGT  
30 GTTTGGGCCTCAAATTATGATTGAGGGGTATCAAACCTCCGAATGTTCAGC  
GCTTCGGAAGAATTGTAGCTCTTAGTACCATTAAATTCTTCGTAGTT  
AGATCAGCTAACTAGCTTAAAGAGATTCTTGGGTATTGGTCAAAATGT  
AGTGAATATTTACTGCTGTTCCCTCTCATTATAGGGTTACTATCCCTAAAG  
CCAAGTTACGGAAATATAAAAGCGTTATATTACTGCTTCTGATGTCTC  
35 TTTCATAGAGTGTACTCAAGTTAGATATTAAATAGATGCTAATCG  
GGTTTTGAAATCGACGATCTATGGACAAATACCTAGGCGGCTTCTA  
CCTATGGAGTTATCGAAACATAAAAGGGTGGCTTCTA  
ACTATTAGAAAATGA  
A

40 (SEQ ID NO: 84)

MLKRLFTEDGELTKISRRFVWMLVVIYCLIIVRMCFGPQIMIEGVSTPNVQRFG  
RIVALLVPFNSFRSLDQLTSFKEILWVIGQNVVNILLFPLIIGLLSLKPSLRKYK  
SVILLAFLMSLFIECTQVVLDILIDANRVFEIDDLWTNTLGGPFALWSYRNIKG  
WLLTIRK\*

Sequence description:

5           A] Length: 516 bp - 172 aa (full-length gene)  
B] ATG start codon is preceded by an Shine-Dalgarno sequence. Possesses a potential leader peptide sequence. C-terminus need further confirmation.

10

ID-118

Clone 3-3

15

(SEQ ID NO: 85)

20

ATGAAAAAGCTTACTTTATTGGGATTAGATGGGACATTAATAGATTG  
TATGTACCAATTATGGAAGCTCTGAAGAACCTATCGTCATTTGGCTTA  
ATATTGATAAAGAATTAATCCATGAATATATTTACAGGAATCAGTGGGG  
CAATTATTGGTAAACCTTCAGAGGAAGAGCAAATACCTCATGAAAAACT  
GAAAGCATATTTACAAAAGAACACAAGAAAGTCGAGATTCTAAAATACATT  
TAATGCCATATGCAAAAGAGATTAGAATGGACCAAAGAACAAAGATATT  
CCCAATTATGTATACACATAAAGGAGCAAGTACGCATTCACTGTTGGAA  
ACCTTGCAGATCTCTCATTATTTGATGAAATTAACTGGTGTTCGGGAT  
TCGAGCGAAAACCACATCCACAAAGGGATTAATTATTTAGTAAACGATATT  
CTTAGATAAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTGG  
AGGTTGCTAAAATGCTGGTATAAAATCCATAAAACTTAAGGTTAGAGAATT  
CCAAAGAAAAACTATAATATTCAAGTCTCAAAGATATAATATCACTTGATT  
TCACTCGTTGGATTAA

30

(SEQ ID NO: 86)

35

MKKLTIFIWLDGLTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGQLL  
VNLSEEEQIPHEKLKAYFTKEQESRDSKIHLMFYAKEILEWTKEQDIPNFMYTH  
KGASTHSVLETQISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYI  
GDRPLDLEVAQNAGIKSINRLLENSKENYNISSLKDIISLDFTRLD\*

Sequence description:

40           A] Length: 627 bp - 209 aa (Possible Full-length gene)  
B] ATG start codon is preceded by an possible Shine-Dalgarno sequence. No obvious leader peptide sequence.

ID-119

Clone 3-7

5

(SEQ ID NO: 87)

ATGGAAAAAGAAAAAAATTAGGTCTTTACCAACTAACAAATGCTTGTCA  
GGCTCTCTTATCGGTGGCGGAATCTTGATTAAATGCAAAATATGAGTTCC  
AGAGCCGGTTGGTACCAATGCTTATTGCTTGGTAATTACTGCTATCGGG  
10 ATGGGAACCTTCGTTAAGTTCAAAATTATCTGAAAAAAGGCCGGAC  
CTAACAGCTGGAATCTTAGTTACGCTAAAGAGGGGTTGGAAACTTATG  
GGATTAACTCTGCATGGGTTATTGGTTATCAGCTGGCTGGAAATGTT  
GCCTACGCTGCACTCTTATTCACTCGGTTATTCTTAAATTCTTG  
GTAATGGAAATAATATCATCTCAATTATTGGAGCAAGTATAGTTATTGGG  
15 TTGTC CATTCTTAATTAAAGAGGTGTTAACAGCTGCATTATTAATAC  
CGTAGTTACCTTGCAAAATTAGTACCTGTTATTATTCTTAATTTCAGCG  
TTATTAGCTTCAAATTAAACATTAGTCTGATATCTGGGAAATGGAT  
TACATCAATCAATTCAACCAAGTCAATTCAACTATGAAAACCGCTGTT  
GGGTATTATTGGTATTGAGGGCGCCGTTCTCAGGTCGTGCTAAAA  
20 AACACTCTGATATTGGTAAAGCAAGTACCTAGCATTTCAGTATGATT  
CACTTATGTATTGATTCTGTTTATCACTGGTATCATGTCACGTCCAGA  
ACTTGCAAACCTAAAAACACCAAGCTATGGCTACGTTAGAAAAAGCTGT  
TGGTCACTGGGTGCTATCTAGTTAACCTGGTGTATCATTCAAGTATT  
GGCGCTATTCTGCTTGGACTTATTGCAGCAGAATTACCATATCAAGCT  
25 GCTAAAGAAGGTGCTTCTAAATTGGCAAAAGAAAATAACAA  
AGCTCCAATCAACTCACTCTAGTCACTAATCTTGTGTACAAGCATTCTA  
ATCACGTTCTTATTCACACAAAGTGCTTATCGTTGGTTGCATTAGCAT  
CATCTGCTATCTTAATTCTTATGCTTACAGCACTATATCAATTACAATT  
CACACTCCGTGAGGATAAGTCAACTCCAGGACATCAAAAGAATTAAATT  
30 TCGGTATCCTCGCTACAATCTATGCTTACCTATCTACGCTGGTGGTT  
TGATTACTTACTTTGACAATGATTGCTTAACTCTAGGTATGATTCTCTAT  
ATTAAAATGAGAAAAGATGACAAGCTGGCGTAATCATGGTCATAGCTGT  
TTCCAGTGTGAAATTGTTATCC

35

(SEQ ID NO: 88)

MEKEKKGLLPLTMLVIGSLIGGGIFDLMQNMSSRAGLVPMLIAWVITAIGMG  
TFVLSFQNLSEKRPDLTAGIFSYAKEGFGNFMGFNSAWGYWLSAWLGNVAY  
AALLFSSLGYFFKFFGNNGNNIISIIGASIVIWVVHFLILRGVNNTAAFI  
LVPVIIFLISALLAFKFNIFSLDIWGNGLHQSIQNSTMKTA  
VWWFIGIEGAV  
40 VFSGRAKKHSIDIGKASILALFTMISLYVLISVLSLGIMSRPELANLKTPAMAYV  
LEKA VGHWGAILVNLGVIISVFGAILAWTLFAAELPYQAAKEGAFPKFFAKEN  
KNKAPINSLLVTNLCVQAFLITFLFTQSA YRFGFALASSAILIPY AFTALYQLQF  
TLREDKSTPGHQKNLIIGILATIYAVYLIYAGGF DYLLTMIA YTLGMILYIKMR  
KDDKLGVIMVIAVSSVKLLS

Sequence description:

5

A] Length: 1356 bp - 452 aa (partial sequence)  
B] ATG start codon is preceded by an possible  
Shine-Dalgarno sequence. Possesses a potential  
leader peptide sequence.

10

ID-120

Clone 3-8

15

(SEQ ID NO: 89)

20

ATGAAATTGAAAAACGGCAGGTCTATTATGTTGTCATAAACATTGCTATT  
TGCTATGCTATACAGGCTTATTGGGGAGCTGTTCTAATATTTAACTACGC  
TTCATAAGGCAATATTCCTTTGATGGGAGCTGGAATTGCCTATATTAT  
TAATATTGTAATGTCAGTCTATGAGCGATTATATATAAAAGCTTTAAAGG  
ATCTAGACTATTAATGGCAATCAAGCGTAGTGTCTATGATTTCCTAT  
GCAACTTTATTGGTTAATTGTCAGTGGCTATTTCATTGTCATTCCAGATT  
TGATTCTAGTTGAGTTCTTATTGGTTATTGATAACGGAGCACTGCTAA  
ATTGGTTAATAATCTCAATGAAAATAACAAATTCTGAGGCTTAAATTAA  
TATGGGAACAGATAAAGACTTAGTTCTACTTTAAGTGGTTATGCCAGCA  
GATTGAAAGCAAGTTTATCTGTTAACAAATTACTAACCTCAGTTCC  
TCTATTGCGGCAACACTCTGAATGTTTGTAGTTATTTCATTGTCATT  
CGTTTGGCAAACAAGGAGCAGTGGGACGTCAATTAAATTGTTAATTGA  
TACCTATTAGGTTCAACAGGCAAAACATTCCATTACGTTGTCATATCCTT  
30  
CATCAACGTTCCATGGTTTTGTAAGCCAAACTTAAAGCTATGATT  
TAGGAAGTTGACGGTTATTGGTATGTTGATCTCCAATTCTTATGCTTT  
AACAGTTGGGTTTAGTTGCTTACAGCTCTAATACCGGTTGTGGGAGC  
CTACATTGGTGTACAATCGGTTCATCTTAATTGCTACTGAATCGCTTACT  
GAAGCATTCTGTTCTTGTACCTTACAACAATTGAGGGAA  
35  
ATGTCATTATCCGAAAGTTGTCGGTGGATCGATTGGACTGCCTCTATGT  
GGGTTTAATGGCTATTACTATCGGAGGTGCTTATGGGGGATCTTAGGCA  
TGTTACTTGCTGTTCTGTCAGCTACTATCTCAGATTGAAAAGATCA  
TATTATCAAGCGACAAACGCTTAGAAATCGTGCACGAACCTATCGTTAA

30

(SEQ ID NO: 90)

MKFEKRQVYYVVITFAICYAIQAYWGAWSNLTLLHKAIFPFLMGAGIAYIINI  
VMSVYERLYIKLFKGSRLLMAIKRSVSMILSYATFIGLIVWLFSIVPDLISSLSS  
LLVIDTGALAKLVNNLNENKQISEALNYMGTDKDLVSTLSGYSQILKQVLSV  
LTNLLTSVSSIAATLLNVFVSFISIYVLANKEQLGRQFNLLIDTYLGSTGKTFH

YVRHILHQRFHGFFVSQTLEAMILGSLTIGMLIFQFPYALTVGVLVAFTALIP  
VVGAYIGVTIGFILIATESLTEAFLFVLFLILLQQFEGNVIYPKVVGGSIGLPSM  
WVLMAITIGGALWGILGMLLAVPVAATIYQIVKDHIKRQTLRNARTYR\*

5

Sequence description:

10

- A] Length: 1134 bp - 378 aa (full-length gene)
- B] ATG start codon is preceded by an typical Shine-Dalgarno sequence. Possesses a potential leader peptide sequence.

15

ID-121

Identical to ID-68, as described in WO 00/06736

20

ID-122

Clone 3-16

25

(SEQ ID NO: 91)

GTGATTACAATTAAAAAGGAATCTGTTATCAAACATTGAAGTATGCTTT  
GGCATTATAATGGGATTATTATCTTAGCTATTGTAATAAGGTGGGCTCCTA  
TTTGCATACTACGTTAGTCGTTCTCCGAAATTAAACCGATCAAGCTTAAAAA  
TCCGTTAACTCTAGTTGGTTATGATGGTAATAATAAACTTATTGCCGATT  
TAGGCTCAGAAAAGCGTAAAGTGTAGTGCAGGATAGCATTCCACTAAAT  
TTGGTTAACGCTATCACTCTATAGAAGATAAACGTTCTTAAACATAGA  
GGTGTGATATTATCGTATTAGGTGCAGCTGGCATAACCTTGTAGTA  
GTAATACGCAAGGTGGTTCAACCCTTGATCAACAGTTGATTAAACTGGCTT  
ACTTTCTACCAATAAAATCTGACCAAACGTTAAACGTAAATCACAGGAA  
GTTTGGCTTGCCTTCAAATGGAGCGTAAATACACCAAAGAAGAAATTCTT  
ACTTTCTATATTAATAAAAGTTATATGGGAAATGGGAATTATGGTATGAGA  
ACAACAGCTAAATCATACTTGGTAAAGACCTAAAGGAATTATCTATTGCA  
CAAATTGCTTGCTCGCTGGTATTCCCTCAAGCACCTACACAATATGACCCTT  
ATAAAAACCCAGAATCTGCTCAAACAAAGACGTAATACCGTTCTCAGCAG  
40 ATGTATCAAGATAAAAACATTCTAAAAAGGAATACGACCAAGCTGTTGC  
AACTCCAGTAACGTGATGGCTAAAAGAATTAAAGCAAAAATCTACTTATCC  
AAAATATATGGATAACTACTTAAACAAAGTTATTAGTGAAGTTAAACAAA  
AAACTGGTAAAGATATCTTACTGCTGGCTAAAAGTGTACTAAATATCA  
ACACTGATGCACAAAAACAACTATGACATCTACAAACAGTGACTTAC

ATCGCTTATCCAAACAATGAATTACAAATAGCATCTACCACATGGATGCG  
ACTAATGGTAAAGTCATTGCACAATTAGGCAGGCGTCATCAGAACGAAAA  
TATTTCATTGGGACAAATCAATCTGTCTAACAGACCGCGATTGGGGTTC  
5 TACAATGAAACCTATCTCAGCTTATGCACCTGCTATTGATAGTGGTGTCTA  
TAATTCAACAGGTCAATCATTAAACGACTCAGTTACTACTGGCCTGGTAC  
TTCTACTCAAATATGACTGGATCGTCAATATATGGGTTGGATGAGTAT  
GCAGACCGCTATTCAACAAATCACGTAACGTCCCTGCTGTCAGAGCACTTGA  
AGCCGCTGGATTAGACGAAGCAAAATCTTCCTGAAAAAATTAGGCATAT  
ACTATCCAGAAATG

10

(SEQ ID NO: 92)

MITIKKESVIKLLKYAFGIIMGFIILAIIVIGGLFAYYVSRSPKLTDQALKSVNSS  
LVYDGNNKLIADLGSEKRESVSADSIPLNLVNAITSIEDKRFFKHRRGVDIYRILG  
AAWHNLVSSNTQGGSTLDQQLIKLAYFSTNKSDQTLKRKSQEVLWALQMER  
15 KYTKEEILTFYINKVYMGNGNYGMRTTAKSYFGKDLKELSIAQLALLAGIPQA  
PTQYDPYKNPESAQTRRNTVLQQMYQDKNISKKEYDQA V ATPVTDGLKELK  
QKSTYPKYMNDYLKQVISEVKQKTGKDIFTAGLKVVYNINTDAQKQLYDIYN  
SDTYIAYPNNELQIASTIMDATNGKVIAQLGGRHQENISFGTNQSVLDRDW  
GSTMKPISAYAPAIDSGVYNSTGQLNSVYYWPGTSQLYDWDQRQYMGWM  
20 SMQTAIQQSRNVPAVRALEAAGLDEAKSFLEKLGIYYPEM

Sequence description:

25

A] Length: 1386 bp - 462 aa (partial sequence)  
B] GTG start codon is preceded by an  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.

30

ID-123

Clone 3-17

35

(SEQ ID NO: 93)

ATGGCTAATGTATATGATTAGCAAATGAATTAGAACGTGCTGTTCTGCT  
TTACCAAGAACCAAGCAGTTAACTGCAAAAGCAGCTATTGAAAATGA  
TGCAGATGCACAAGTGCTTGGCAAGACTTTGGCTACCCAAATCAAAAGT  
40 TCAAGAAATGATGCAATCTGCCAAATGCCAAGTCAAGAAGAACAAAGATG  
AAATGTCTAAACTGGGGAAAAAAATTGAATCCAATGACCTTTAAAAGTT  
ATTGGACCAACAACACGGTTGTCTGTCTATGTCTGATATCGAAAAAA  
TTGTCTTGCACCCATGCAGGACTTGATGTAA

(SEQ ID NO: 94)

MANVYDLANELERAVRALPEYQAVLTAKAAIENDADAQVLWQDFLATQSK  
VQEMMQSGQMPSQEEQDEMMSKLGEKIESNDLLKVYFDQQQRLSVYMSDIEKI  
VFAPMQDLM\*

5

Sequence description:

- 10 A] Length: 336 bp - 112 aa (full length sequence)  
B] ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. No obvious  
potential leader peptide sequence.

15

ID-124

Clone 3-26

20 (SEQ ID NO: 95)  
ATGGCAGAAATCACAGCTAAACTGTAAAAGAATTGCGTGAAAAATCAGG  
TGCAGGCCTATGGACGCTAAAAAGCATTAGTAGAAACTGATGGTGACC  
TTGATAAAGCGATTGAATTACTTCGCGAAAAAGGTATGGCTAAAGCAGCT  
AAAAAAAGCAGACCGTGTGCTGCTGAAGGTTAACAGGTGTTATGTTGAT  
25 GGTAACGTTGCAGCAGTTATTGAAGTTAA

(SEQ ID NO: 96)

MAEITAKLVKELREKSGAGVMDAKKALVETDGDLDAKIELLREKGMAKA  
KADRVAAEGLTGVYVDGNVAAVIEV

30

Sequence description:

- 35 A] Length: 230 bp - 76 aa (partial sequence)  
B] ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. No obvious  
potential leader peptide sequence.

40

ID-125

Clone 3-33

(SEQ ID NO: 97)

ATGATAAAAAACCTGTTATTAAACAGGTTTTATCATTAAATGACGGAAAA  
CTGGACACAAATTATTTCTGTATAATTAAATATTATTTCTTATCAGG  
AGGTTATGATGACATTAGAGAAACGATTAA

5

(SEQ ID NO: 98)

MIKNLLTGFLSFNDGKLDTNYFSCIKYIISYQEVMMTLEKRF

10 Sequence description:

A] Length: 134 bp - 44 aa (partial sequence)

B] ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. Possible  
potential leader peptide sequence.

15

ID-126

20 Clone 3-41

(SEQ ID NO: 99)

ATGAAAAATAATAAAAATAATGGTTTCTGAAAAATTCCCTTATTTACATA  
TTATTGATTATTGCGGTATTACAACCTTCAATACTATTAA

25

(SEQ ID NO: 100)

MKNNKNNGFLKNSFIYILLIAVITTFQYYL

30 Sequence description:

A] Length: 94 bp - 31 aa (partial sequence)

B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

35

ID-127

40 Clone 3-42

(SEQ ID NO: 101)

ATGTTAGATATTATCTTATCCGGAATTCGCAAGGATTACTTGGTCAATT  
TGGCAATTGGCGTGTATCACTTTCGTATCTTAGACATAGCCGATCTCTC

TGCAGAAGGGCTTCCCTATGGGGCTGCAGTTGCGCCTATGTATCGT  
TAA

(SEQ ID NO: 102)

5 MLDIILSGISQGLLWSIMAIGVFITFRILDIA DLSAEGAFPMGA AAVCALCIV

Sequence description:

10 A] Length: 158 bp - 52 aa (partial sequence)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

15 ID-128

Clone 3-43

20 (SEQ ID NO: 103)  
ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTAAAATGAG  
TATTGATAAACTTAGATATAAAGAACCA CAGAGTGAACATGACAAGCGAC  
CTACTTTTATTGGTAGTACTTATACTGTTACTGTAGCAGTTATATTGTC  
GTTATTAA

25 (SEQ ID NO: 104)  
MEMPKRNELLNKEIKMSIDKLRYKEPESEHDKRPTFYLVVLILVTAVILSLF

30 Sequence description:

35 A] Length: 161 bp - 53 aa (full-length gene)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

ID-129

40 Clone 3-44

(SEQ ID NO: 105)

GTGGTAAGTAAATTGAGTTAACAAACGATTTGCATTGCTATTTCATCA  
ATGCTAATTACGCAACACACCTCTATCTTACAAGTATTGGGGAACCTTC

TCTGAACGTGGTGGTATCGCAACGTTGGTTAGAAGGAATTATGGTAATT  
GGAGCTTCTCAGGC GTTGTATTAA

(SEQ ID NO: 106)

5 MVS KLSLTTIFALLFSSMLIYATPLIFTSIGGTF SERGGIVNVGLEGIMVIGAFSG  
VVF

Sequence description:

10

A] Length: 179 bp - 59 aa (partial sequence)  
B] GTG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

15

ID-130

Clone 3-46/47

20

(SEQ ID NO: 107)

ATGAGAATTATTGCAATAACTGAAAAGGTTATAAAAGAACTGTT CGTGAT  
AAAAGAACACTTGCTATGATGTTTAGCACCTATTTAATTATGTTTG  
TGAATGTTATGTTCTCGAATAGTAATACAAAAGTTAAGATTGGA ACTA  
25 TTAACGTTAACACGAAGGTCGTTCAAATTAGATAATATTAAGCATATT  
AAGTGAGATCATTAAATTAACTCATCTGCTAAAAAGCACTCAAATCAA  
ATAAAATTGATGCTCTTATT CGGAGGACAATAAATCTTATACTGTCT  
ATGCGAATACAGATTCTCAAAGACGACTTTAACAAAGACAAGCTTTAAA  
30 ACCGCTGTTAACATGAACAGTAAGGAACTGATT CGCAAGTTAAAATT  
TTAGCTAATAAGAATCCGAAACTAGCACAATCCTAACAAACTCGCTCCAAA  
TATATCAAAGAAAAATATAATTACGGAAATAAAATACAGGCTTTTGC  
AAAAATGATACCAATACTAATGGGATTATGGTCTTCTGGTTTT

(SEQ ID NO: 108)

35 MRIIAITEKVIKELFRDKRTLAMMFLAPILIMFLMNVMFSANSNTKVIGTINV  
NTKVVSNLDNIKHIQVRSFKFNSSAKKALKSNKIDALISEDNKSYTVFYANTDS  
SKTTLTRQAFKTA VNTMNSKELISQVKILANKNPKLAQSLQTRS KYIKEKYN  
GNKNTGFFAKMIPILMGFMVFFLVE

40

Sequence description:

A] Length: 558 bp - 186 aa (partial sequence)  
B] ATG start codon is preceded by a

possible Shine-Dalgarno sequence. Potential leader peptide sequence. C-terminus has yet to be determined.

5

ID-131

Clone 3-48

10

(SEQ ID NO: 109)

GTGATTATCGTTATGAGTAAACATCAAGAAATTTGGAGTACCTAGAAAAT  
TTAGCTGTTGGTAAGAGGGTTAGTGTACGCAGTATTCAAATCATTAA

15

(SEQ ID NO: 110)

MIIVMSKHQEILEYLENLAVGKRVSVRSISNHL

Sequence description:

20

A] Length: 100 bp - 33 aa (partial sequence)

B] GTG start codon is not preceded by a  
obvious Shine-Dalgarno sequence. No obvious  
leader peptide sequence.

25

ID-132

Clone 2-c53

30

(SEQ ID NO: 111)

ATGTATAGAGAAATTACCGCTGTCGAACACGATCGCTTGTGAGCGAATCC  
AACCAAACAAACCTACTTCAATCTCTTAATTGGCCCAAAGTAAAAGACAA  
CTGGGGTAGTCAATTACTGGCTTTGACGGTGAAACCCAAATTGCCAG  
CGCTAGTATTCTCATCAAATCACTCCTCTGGCTCTCCATGCTGTATATT  
35 CCGCGTGGACCAATCATGGATTACTCCAATCTAGATATTGTAACTAAGGTC  
CTTAAGGACCTTAAAGCTTTGGAAAAAACAAAGAGCTCTTTATCAAG  
TGTGATCCTCTCATCTATT

40

(SEQ ID NO: 112)

MYREITAVEHDRFVSESNQTNLQLQSLNWPKVKDWNWGSQLLGFFDGETQIASA  
SILIKSLPLGFSMLYIPRGPIMDYSNLDIVTKVLKDLKAFGKKQRALFIKCDPLI  
Y

Sequence description:

5           A] Length: 326 bp - 108 aa (partial sequence)  
B] ATG start codon is preceded by an obvious  
Shine-Dalgarno sequence. No obvious leader  
peptide sequence.

10           ID-133

Clone 2-c59

15           (SEQ ID NO: 113)  
ATGGACAAGAAAAAAATCTTAGTAACGGGTATTGTGCCTAAAGAAGGTCT  
AAGAAAGCTTATGGACCGATTGATGTTACTTATTCAAGAGATCGCCCATT  
TTCACGTGACTATGTGTTAGAGCATTATCTGAATATGACGGATGGTTACT  
CATGGGACAAAAAGGTGATAAAGAGATGATTGATGCAGGTGAAAACCTAC  
20           AAATTATTCCTT

25           (SEQ ID NO: 114)  
MDKKKILVTGIVPKEGLRKLMDRFDVTYSEDRPFSRDYVLEHLSEYDGWLLM  
GQKGDKEMIDAGENLQIIS

Sequence description:

30           A] Length: 215 bp - 71 aa (partial sequence)  
B] ATG start codon is preceded by an obvious  
Shine-Dalgarno sequence. No obvious leader  
peptide sequence.

35           ID-134

Clone 2-c62

40           (SEQ ID NO: 115)  
ATTCGAAAGATGACTACCAAAATATTAGTTGGACAGGATCCAGAAGTT  
GTTGATTATGCTGGTCTGTTGAAAAACGCCGTCCAGTTAGAAAAAGCA  
GTTAAAAATTCTTGCAAGAAGAGAGAGCTACGAGAATGCTATCTGATTTC  
TTGCAAGAAGAAAAATGGGTAAGTATTGCTGAATTATGGCGATCAA

AGAACATTTGTAATAAGGCCTCAAGAATGGATGACAAGGCTATTA  
TACGCCCGAAGAAGAAGCCTAGCAGGATATCGTCAAAAGCTTAGTGAA  
GTGATAAAAATATCATGAAGTAACGCAATATTCTTTACAAACAATGGTT  
5 GAGTTAAAAGAATATGCTAATGATAAAGGGATTCAAATTATCGGTGATAT  
GCCAATCTACGTTCTGCCGATAGTAGAAGTTGGACAATGCCTGA  
GTTC

(SEQ ID NO: 116)

ISKDDYQNIISFGQDPEVVDYAGLFEKRRPVLEKAVKNFLQEERATRMLSDLQ  
10 EEKWVTDFAEFMAIKEHFGNKALQEWDKAIIRREEALAGYRQKLSEVIKY  
HEVTQYFFYKQWFELKEYANDKGIIQIIGDMPIYVSADSVEVWTMPELF

A] Length: 459 bp - 153 aa (partial sequence)

15 B] More sequencing is required to determine the  
N- and C-termini  
enzyme). - Streptococcus pneumoniae (63%)

20 ID-135

Identical to ID-108 described in WO 00/06736

Clone 2-c63

25

ID-136

Clone 2-c66

30

(SEQ ID NO: 117)

ATGGCAAAACAGAAAAATAACTGGGCCGTGTTGGAGTTGGTGTCCCTAC  
ACTTGCTTCAGTTGCGACTCTGCTGCATGTGGAAGTAAATCAGCTCCCA  
GGATTCTAATGGAGCGATTAATTGGGCTATTCCAACAGAAATCAATACACT  
35 AGATTATCTAAAGTTACAGACACTTACTCAAATCTAGCTATTGGTAAC  
TAGTAGTAATTCCCTCGCTTAGATAAAGATGGAAAGACAAGACCAGACTT  
GGCTACTAAAGTTGATGTTCAAAAGATGGCTTAACCTATACAGCTACATT  
ACGTAAAGGCTTGAAGTGGCAGATGGCAGTAAACTTACTGCAAAGGATT  
TTGTTTATTCACTGGCACACGTTAGTTGATCCTAAAACAGCTTCACAATATG  
40 CTTACCTTGCTGTTGAAGGGCATGTGCTTAATGCCATAAAATCAACGAAG  
GACAAGAGAAAGACTTGAATAAGCTAGGTGTTAAGGCAGAAGGCGATGA  
CAAAGTTGTTATTACTTATCTAGTCCGTCTCCGCAATTCACTACTACCTT  
GCATTCACTAATTCACTGCCACAAAAACAAGAAGTTGTTGAAAAATATGG  
AAAAGATTACGCAACTACTCAAAAAATACAGTTACTCAGGACCATA

CTGTTGAAGGTTGGAATGGTTCGAATGGTACCTTCACGCTGAAGAAAAAC  
5 AAAAATTATTGGGACGCTAAAAATGTAAAAACAAAAGAAGTCGCATCCA  
GAATGTTAAAAACCAGATACCGCCGTTCAAATGTATAAACGTGGTGAGT  
TAGATGCAGCTAATATCTCAAATACTTCTGCTATTATCAAGCTAATAAAA  
ATAATAAAAGATGTCACAGATGTTCTAGAAGCGACCACTGCCTATATGGAA  
TATAATACTACTGGTTCTGTGAAAGGGCTTGATAATGTTAAGATTGTCGC  
10 GCCTTAAACTTAGCAACTAACCGTAAAGGAGTTGTTCAAGCAGCCGTTGAT  
ACAGGCTAAAACCGGCAATTGCTTGCACCTACTGGTTAGCCAAAACA  
CCAGATGGAACTGATTGGAAAATATGTTGCCAGGTTATGAATATAAT  
AAAAGTGAAGCAGCAAAACTCTTAGACTA

(SEQ ID NO: 118)

MAKQKNNWRRVGVLTLASVATLAACGSKSASQDSNGAINWAIPIEINTLD  
LSKVTDTSNLAIGNSSSNFLRLDKDGKTRPDLATKVDVSKDGLTYATLRKG  
15 LKWSDGSKLTAKDFVYSWQRLVDPKTASQYAYLAVEGHVLNADKINEGQEK  
DLNKLGVKAEGDDKVITLSSPSPQFIYYLAFTNFMPQKQEVEKYGKDYAT  
TSKNTVYSGPYTVEGWNGSNGTFTLKKKNKNYWDANKVTKEVRIQTVKKPD  
TAVQMYKRGEELDAANISNTSAIYQANKNNKDVTDVLEATTAYMEYNTTGSV  
20 KGLDNVKIRRALNLATNRKGVVQAAVDTGSKPAIAFAPTGLAKTPDGTDLAK  
YVAPGYEYNKTEAAKLFRL

Sequence description:

25

- A] Length: 1143 bp - 381 aa (partial sequence)
- B] Shine-Dalgarno sequence precedes ATG codon.  
Possesses a potential leader peptide sequence.

30

ID-137

Clone 2-c67

35

(SEQ ID NO: 119)

TTGAGAGTTATGAAAATAAAGAAGAGTTGAAAAAGAAAATAAGTAAAAC  
ATTGAGAAATACATTATGGAATTAAATAA  
TATTCCAGAGAATCTAAAAGATAAAAGAATTGATGAAGTTGATAGAACTC  
CAGCAGAAAACCTTCTTATCAGGTTGGCT  
40 GGACCAACTTGGTTCTTAAATGGGAAGAAGATGAAAGAAAGGGACTTCAA  
GTAAAAAACACCATCGGATAAATT

(SEQ ID NO: 120)

MRVYENKEELKKEISKTFEKYIMEFNNIPNLKDKRIDEVDRTPAENLSYQVG  
WTNLVLKWEEDERKGLQVKTPSDKF

5

Sequence description

A] Length: 234 bp - 78 aa (partial sequence)

10 B] TTG start codon is preceded by a  
potential Shine-Dalgarno sequence. No obvious  
leader peptide sequence.

15 ID-138

Clone 2-c70

(SEQ ID NO: 121)

20 ATGTCAAAGTTGATAGTCAGAAAATAATTACTCCGATTATGAAGTTGTC.  
AATATGCGAGGGATTATTGCACTCAAAGATGGCATGCTAGCAATTACCA  
CTAACAGTTGGAGTCTCTTTAATATTAGGGCAGCTTCCATT

(SEQ ID NO: 122)

25 MSKFDSQKIIITPIMKFVNMRGIIALKDGMLAILPLTVVGSLFLILGQLPF

Sequence description

30 A] Length: 150 bp - 50 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
Shine-Dalgarno sequence. Possesses a potential  
leader peptide sequence.

35

ID-139

Clone 2-c71

(SEQ ID NO: 123)

40 GAGACCACCTTCATCAGTTAAACCAGCAGGAATTGACCGTATCAATCATA  
TCAACACCCCCGAAGAAAACTACCCCCAACATTGCAACGACGCATAGCTT  
CAAAGATCGTTGTGATACTTAGAAAGAATTACAATGAAGACATTGATGT  
TTGTTCTGGATTCAATTGTGGTATGGGAGAGAGCGATGAGGGGCTCATCAC

ATTAGCTTCAGACTAAAAGAACTGAACCCCTATTCTATCCCTGTCAATT  
TTACTTGCTGTTGAAGGAACACCTCTGGAAAATAACTATTGACTCCC  
5 ATTAATGCTTAAAAATTATGCCATGTTGCCTTGTGTTCAAGG  
AATTAAGATTAAGTGCTGGACGGGAGGTCCATTGAGAATTGAAATCAT  
TAGTCACCTTACTTGTGACTCAACTTTGGAAATTACCTAACAGAGG  
GGGGTCGCAATCACACATACCGATATTGAATTCTGGAAAAATTACAAC  
AATCATACTAAAAAGGAATTAATT

(SEQ ID NO: 124)

10 ETTSSVKPAGIDRINHTSTPPKKTPNIATHSFKDRCDTLERIH  
NEDIDVCSGFI  
CGMGESDEGLITLAFRLKELNPYSIPVNFLAVEGTPLGKYN  
YLTPIKCLKIMA  
MLRFVFPFKELRLSAGREVHFENFESLV  
TLLVDSTFLGN  
YLT  
EGGRNQH  
TDIEF  
LEKLQLNHTKKELI

15

Sequence description:

20 A] Length: 535 bp - 178 aa (partial sequence)

B] N- and C-termini require verification

ID-140

25

Clone 2-c73

(SEQ ID NO: 125)

30 ATGCCGGTTGGACTGCACAGTCTATTCAAAGGCATTAGAAAAGCAT  
AATACTAAGGAAGGCACCTGGGAAA  
ACTAACCACTTAAGTGGTTCTTA  
GTATTACCAAGTTATCTCCTGATGGAGAGGAA  
ATCTCGCGGCATATT  
GATGCTAGTAGTGATATT  
CCTTGTGATCCACAAGTCTGGCATAAAGTT  
TCGCCGAATAGTCCAGACTTAAGTTGCTATCTAAC  
TTTACTGCCAAAAAA  
GAAGATTACTCCATAAAAAA  
ATGGTCTCACGCGCACACATTCTGAGGTT  
ATCGCCAGTGCACCTCTCTTATCTGAGAAGAGTA  
ATATTAGACCTGGG  
35 TGTGGTCAAGGGCGAAACTCACTTATTATCGCTGCTGGACATCAAGTG  
ACTTCTGTCGATTCAAACGGACAGAGCCTGTAGCTT  
AGAAAATATGGCA  
TTAGAAGAAGAGCTCCTACA  
ATATAAAAAGGTATGATATTAA  
ACTACT  
GCTATTGAAGGGCACTATGATT  
TATTATCAACTGTGGTATT  
ATGTTT  
T

40

(SEQ ID NO: 126)

MPVWTAQSIPKA  
FLEKHNTKEGTWAKL  
TILSGSLVFYQLSPD  
GEISRHIFDAS  
SDIPFVDPQVWHKV  
SPNPDLS  
CYLTFYCQKEDYFH  
KKYGLTRTHSEVI  
ASAP

LLSEKSNILDLGCGQGRNSLYLSLLGHQVTSVDSNGQLVALENMALEEEELPY  
NIKRYDINTTAIEGHYDFILSTVVFMF

5 Sequence description:

- A] Length: 563 bp - 187 aa (partial sequence)  
B] N- and C-termini require verification

10

ID-141

Clone 2c76

15

(SEQ ID NO: 127)

ATGACAAAGCAAATAATTGCCATTGGGGCTGAAGATGAAGACCATTGAT  
TGGAGTTAATGGCGGTTACCATGGAGGCTTCCTAAAGAGTTACATCACTT  
CAAAGAACGACCATGGGCAGGCTTGCTTATGGGACGAAAGACCTTG  
20 ATGGAATGAACCGTCGTACCTGGTAGAGAGACAATCATCTAACAA  
AAGATGAACAATTCCAAGCAGATGGAGTGACAGTCCTAAATAGTGGAA  
CAAGTTATAAAATGGTTCAAGAACATAATAAGACCTTATTATTGTAGGT  
GGTGCAAGTATTATAAAAGCATTCTGCCTTATTGTGAAGCAATCATAAAA  
ACTAAAGTTCATGGAAAATTCAAAGGTGATACCTATTTCTGATGTTAAT  
25 CTATCTGAGTT

(SEQ ID NO: 128)

MTKQIIAIWAEDEDHLIGVNGLPWRLPKELHHFKETTMGQALLMGRKTFDG  
MNRRVLPGRETIILTKEQFQADGVTVLNSVEQVIKWFQEHNKTLFIVGGASI  
30 YKAFLPYCEAIITKVHGKFKGDTYFPDVNLSEF

Sequence description:

35

- A] Length: 417 bp - 139 aa (partial sequence)  
B] ATG start codon is preceded by a Shine-Dalgarno sequence. No leader peptide sequence

40

ID-142

Clone 2-c78

(SEQ ID NO: 129)

TTGTGGCCAAACTGTGCCCGCTTATTAATAGCACTTGTCACCATTGAA  
GATATCTAACATCAGGTGCTCATAGCAACCCATTAAATGGGGGTTATA  
5 CTTGGCGGGACAATTGTAGTAGTGGCGACAGCACCACTTCTATGGCA  
TTGACAGCTATGCTAGGATTAACCGGAATGCCTATGGCTATAGGAGCCTG  
TCTGTCTTGGTCGTATTATGAATGGGTACTTTCCATAAATTAAAAC  
TTGGAAGTCGTAAAGATAATATAGCTTTGCTGTTGAGCCTCTAACTCAAG  
10 CTGACGTGACTTCAGCTAACCCATTCCAATCTATGTCACTAATTTGTTGG  
TGGTGCAGCTTGGTATTAAATTGCCTGATGAAATTAGTTAATGATACT  
CCTGGAACAGCGACACCAATTGCAGGATTGCTGTCATGTTGCCTATAAC  
CCAATGATAAAAGTACTAATAACCGCTCTAGGTTGTATTATCCTATCTTA  
CTAGCAGGCTATTGGAGGCATTGTTTT

(SEQ ID NO: 130)

15 MWPNCAPLINSTLFTIEDILTSAGHSNPILMGVILGGTIVVVATAPLSSMALTA  
MLGLTGMPMAIGALSVFGSSFMNGVLFHKLKLGSRKDNIAFAVEPLTQADVT  
SANPIPIYVTNFVGGAACGILIALMKLVNDTPGTATPIAGFAVMFAYNPMIKVL  
ITALGCIILSLLAGYFGGIVF

20

Sequence description:

25 A] Length: 540 bp - 180 aa (partial sequence)

B] N- and C-termini have yet to be elucidated

ID-143

30

Clone 2-c80

(SEQ ID NO: 131)

35 ATGTTTTAAGTATAATGGCAGGTGTCATAGCATTGTCCTGACAGTTATT  
GCCATTCCACGCTTCATTAAGTTACCAATTGAAGAAAATTGGCGGGCAA  
CAAATGCATGAAGATGTCAAACAAACATCTAGCCAAAGCAGGTACGCCGAC  
AATGGGAGGAACGGTATT

(SEQ ID NO: 132)

40 MFLSIMAGVIAFVLTVIAIPRFIKFYQLKKIGGQQMHEDVKQHLAKAGTPTMG-  
GTVF

Sequence description:

5

- A] Length: 172 bp - 57 aa (partial sequence)  
B] Shine Dalgarno sequence precedes 'ATG' start codon. Possesses a potential leader peptide sequence.

#### ID-144

10 Clone 3-83

(SEQ ID NO: 133)

ATGAAACCATAATTATCTTTATTGGTAGAACGTTATTATACTTCGGTATT  
TATTGTTACTAATTACTTTGCATACCTTGGTCGGACAAGGCAGTT  
15 TATTATAAA

(SEQ ID NO: 134)

MKPYLSFIGRTLLYFGILLLIYFFAYLGRGQGSFIY

20

Sequence description:

25

- A] Length: 113 bp - 37 aa (partial sequence)  
B] Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possesses a potential leader peptide sequence.  
This orf is not in frame with nuc

30

#### ID-145

Clone 3-86

35

(SEQ ID NO: 135)

ATGTCATATTTAGAAATTACTGGTATCGTTGGAGCAATTATTATTAA  
TTTAGCAGTAATATTGCTTGTAGACCTGACTGGTCAATGCTTCACTA  
TCTATTGTATTTACTTATGGCACTCTAGCGCATCAATTGAAGAATAT  
CAGTTCCCGTGCCCCATCACCTATCATTAACTATGTTGTTATGATGAA  
40 GAAGAGCTGATGGATTGTTCCAGGCAAACTCAGTCTATTATGTTGGTT  
AATACTATTGCTTGGTTGCTTACATTGCTAGTATTGCTTCTCAAGCTT  
ATTGGCTTGGATTAGGAGTCATGTTCTTAGTCTAACGCGAGCTCTGGGTC  
ATGGTTTCAGATGAATATTAACCTAAAACCTGGTATAATCCTGGTCTAG  
CAACGACAGTATTCTCCTAGTACCAATAGCTTGCGCATACATCTATCAAG

CTAGTGCAGAAGGAATGCTCACTGGGGAGATTGGCTAGGTGGTTTATCA  
TGTTGATTGTCTGTACTAACTAGCATTATTGCACCTGTACAGCTATTGAA  
GGATAAGGAGACCAATTATATTATTAGTCCTGGCAAATGGACC GTTTCA  
TAAGGTCGTTAATTTGTAAGGATAAAAAAATAA

5

(SEQ ID NO: 136)

MSYFRNYWYRFGAILFIILAVILLVFRPDWSMLHYLLYFYFMALLAHQFEEYQ  
FPGGASPIINYVVYDEEELMDCFPGNTQSIMLVNTIAWLLYIASIAFPQAYWLG  
LGVMFFSLTQLLGHGFQMNIKLKTWYNPGLATTVFLVPIACAYIYQASAEG  
10 MLTWGDWLGGFIMLIVCVLTSIIAPVQLLKDKETNYIISPWQMDRFHKVVNFV  
RIKK\*

10

Sequence description:

15

A] Length: 651 bp - 219 aa (full length gene)

20

B] Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possesses a potential leader peptide sequence.

ID-146

25

Clone 3-c88

(SEQ ID NO: 137)

ATGCCACTTACAGCACTTGAAATTAAAGATAAAACATTTCATCAAAATT  
CGCGGTTATAGCGAAGAAGAAGTT

30

(SEQ ID NO: 138)

MPLTALEIKDKTFSSKFRGYSEEEV

35

Sequence description:

40

A] Length: 75 bp - 25 aa (partial sequence)

B] Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. No leader peptide

ID-147

Clone 3-90

(SEQ ID NO: 139)  
5 ATGTCACTTTCAAGAAAAATTGCTTACAATTGCGCTAAAAAGGAAGCG  
CTTTATAAAAGAGAGTTAGGACGCTACGCCCTGAGATCAATGCTAGCAGG  
GGCTTATTGACAATGAGTACTGCTGCCGGTATCGTCGCAGCTGATACTAT  
TGGTAAAATTCTCCTGCTCTACAGGTTTGATTGCTTCATCTTAGTT  
10 TTGGACTTATTATGTTTAATATTAATGGTGAATTGGCGACATCTAATAT  
GCTTATCTCACTGCAGGAGCCTATAATAAAATATCTCTGGAAAAAGC  
CATAACAAATTAAATTATTGTACTTTCAACCTCGTTGGCTGTATA  
TTAGCTGGTTGTTAA

(SEQ ID NO: 140)  
15 MSLFQEKIAYNCACKEALYKESLGRYALRSMLAGAYLTMSTAAGIVAADTIG  
KISPALSGFVFAFIFSFGGLIYVLIFNGELATSNMLYLTAGAYNKNISWKKAITILI  
YCTFFNLVGACILAWLF

20 Sequence description

A] Length: 406 bp - 125 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
25 typical Shine-Dalgarno sequence. Possible  
leader peptide

ID-148

30 Clone 3-92

(SEQ ID NO: 141)  
AAGTTACAAGCGACTGAAGTTAAGAGCGTCCGGTAGCACACCAGCTTC  
35 AACAAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCAACCTC  
ATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAA  
TTCAGTACATACCGTGGGGAGATCCAGGTGATCATGGTAAAGGTTAGC  
AGTTGACTTATTGTAGGTAAAAACCAAGCACTGGTAATGAAGTTGCACA  
40 GTACTCTACACAAAATATGGCAGCAAATAACATTGATATGTTATCTGGCA  
ACAAAAGTTTATTCAAATACAAATAGTATTATGGACCTGCTAATACTTG  
GAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACATGACCACGT  
TCACGTATCATTAA

(SEQ ID NO: 142)

KLQATEVKSVPVAQPASTTNAVAAHPENAGLQPHVAAAYKEKVASTYGVNEF  
STYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQ  
KFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSF

5

Sequence description

- 10           A] Length: 419 bp - 139 aa (partial sequence)  
          B] N- and C-termini have yet to be determined

ID-149

15

Clone 3-94

(SEQ ID NO: 143)

ATGATTCCAGTAGTTATTGAACAAACAAGTCGTGGTGAACGTTCTTATGAT  
20        ATTACTCACGTCTTTAAAAGATCGTATTATTATGTTGACAGGCCAAGTT  
          GAGGATAATATGGCCAATAGTATCATTGCACAGTTATTGTTCTCGATGCA  
          CAAGATAATACAAAGGATATTACCTTATGTCAATACACCAGGTGGTTCA  
          GTATCGGCTGGACTTGCTATTGTGGACACCATGAACCTCATTAAATCGGAC  
          GTACAGACGATTGTTATGGGGATGGCTGCTCGATGGGAACCATTATTGCT  
25        TCAAGTGGTCTAAAGGAAAACGTTTATGTTACCGAATGCAGAATATATG  
          ATCCACCAACCAATGGCGGAACAGGCGGAGGTACACAGCAATCTGATAT  
          GGCTATCGCTGCTGAGCATCTTTAAAAACGCGTCATACTTAGAAAAAAAT  
          CTTAGCTGATAATTCTGGTCAATCTATTGAAAAAGTCCATGATGATGCAGA  
          GCGTGATCGTTGGATGAGTGCTCAAGAACACTGATTATGGCTTATTGAT  
30        GCTATTATGGAAAATAATAATTACAATAATAGATTAAAAGAGTTGAGTT  
          TACCAACTCTTTATTGTTGGAATTATGTTATAATCTTAGTAATTACA  
          GATATGACGCAGAAAGGAAAAATTATTGA

(SEQ ID NO: 144)

35        MIPVVIEQTSRGERSYDIYSRLLKDRIIMLTGQVEDNMANSIIAQLLFLDAQDN  
          TKDIYLYVNTPGGSVSAGLAIVDTMNFIKSDVQTIVMGMAASMGTIASSGAK  
          GKRFMLPNAEYMIHQPMGGTGGGTQQSDMAIAAEHLLKTRHTLEKILADNSG  
          QSIEKVHDDAERDRWMSAQEHЛИALLMLWKIIIYNRFRKRVEFTNSFFICW  
          NYVIIIЛVITDMTQKGKNY\*

40

Sequence description

5

A] Length: 693 bp - 231 aa (full length gene)  
B] Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. No leader peptide. Significantly, it would appear to have a very hydrophobic C-terminus.

ID-150

10

Clone 2-c86

(SEQ ID NO: 145)

15

ATGAAACCAAAAaTTATTGGTGTACTGGTCTAGGAATATTGGACAAACA  
CTCGCACAAAGAACTAAGTAACCTTGAACAAAGATGTTATTGCTATTGACAGC  
AATCCTGAAAATGTACAAGCTGTCGCCGAAGT  
TGTTACAAAAGCAGCTATCGGAGACATTACTGATTAGCTTCCTAAAACA  
CATCGGGATCAGTGACTGTGATACTGTTATTATTGCTACAGGAAACAGTT  
AGAGAGCTCAGTATTGGCCGTAATGCACTGTAAAAAGTTAGGCGTCCCAC  
AAGTTATTGCTAAAGCTCGAAACCTTGTATACGAAGAAGTACTTTATGAAA  
20 TTGGTGTGATTGGTTATCTCTCCGGAGCGAGAATCTGGGAAAATGTTG  
CTGCAAACCTCATGAGAAATAAAATTACAGATGTCTTCCAGATTGAATCTG  
ATATTCTGTCATTGAATT

20

(SEQ ID NO: 146)

25

MKPKIIGVLGLGIFGQTLAQELSNFEQDVIAIDSNPENVQAVAEVVTKAAIGDI  
TDLAFLKHIGISDCDTVIIATGNSLE  
SSVLAVMHCKKLGPQVIAKARNLVYEEVLYEIGADLVISPERESGQNVAAN  
LMRNKITDVFQIESDISVIEF

30

Sequence description:

35

A] Length: 459 bp - 153 aa (partial sequence)  
B] Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possesses a potential leader peptide sequence.  
This orf is not in frame with nuc

40

ID-151

Clone 2-c88

(SEQ ID NO: 147)

GTGCGTTATAGTAAAGAGATTATTCAGTTAGCTATACCAAGCTATGATTGAA  
AATATCTTACAAATGCTCATGGGAGTAGTTGATAATTATCTAGTGGCTCAG  
5 TAGGTGTTGTTAGCAGTATCAGGTGTTCAGTTGCTAATAATATAATTACT  
ATTATCAAGCTATTTTATAGCTTAGGGGCAGTATAGCAAGTCTATTG  
GCCAAGTCGTTAGCAGGTAGTGAGAAGGATGATGCAATTTCAGTATGTTCT  
CAAGCCATTTCTAACATCACTGATAGGGCAGTATTAGGAATTATCTCG  
ATTGTTTGGACAAACTTCTT

10 (SEQ ID NO: 148)

MRYSKEIIQLAIPAMIENILQMLMGVVDNYLVAQLGVVAVSGVSVANNIITIY  
QAIFIALGASIASLLAKSLAGSEKDDAISVCSQAIFLTSLIGAVLGIISIVFGQTFF

15 Sequence description

A] Length: 330 bp - 110 aa (partial sequence)

20 B] Putative GTG start codon is preceded by a  
typical Shine-Dalgarno sequence. May have a  
leader peptide

ID-152

25

Clone 2-c92

(SEQ ID NO: 149)

TTGATTAACAAGTATTCTGTGCTTTGAAGAGGGATTCTCCATAATAACT  
30 CCTTTAATAGTTATCGTGAGAAGTATTAAAGAAAAACCGCCAAGGTAG  
AGCGACATTCTGCCTTAACtACAATAAAACCAAGAGAATTAGCACAAC  
ATTATCTCTCAAAATTACAAAGTTCTCAAGGGTTTTAGGAATAGCTAGTG  
AATTGGTAACCTATGATCAACGCTTGTCAAACATT

35 (SEQ ID NO: 150)

MINKYSCFLKRILHNNTPLIVIVRSILKKNRQGRATFLPLTTIKPRELAQHYLSK  
LQSSQGFLGIASELVTYDQRLSNIF

40 Sequence description

A] Length: 240 bp - 80 aa (partial sequence)

B] No obvious Shine Dalgarno sequence precedes the Putative TTG start codon

1 ID-153

5 Clone 2-c94

(SEQ ID NO: 151)

TTGTTGACTCACAAAAATATTATTAAACCATTATTTGGATTATTATGA  
10 TTATATTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATA  
ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAAT  
ACTTTGTTCTATGGGATTGAAAGTCGTTCTGGTACTATAACGGCTTG  
15 ATATTGATTAGCTAATGCTGTTAAAGAACCGGTATTCAGTGAAAT  
GGCAGCCTATTAACGGGATATGAAAGAAACTGAACCTAATAATGGTAAT  
ATAGACCTTATTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAA  
AGTCGCTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAA  
20 AACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGGAAAAACTAG  
GAGCCCAGTCGGGTTCATCTGGTTTGATGCTTTAACGCTAACCTGATA  
TTTAAAAAAAGTTGAAAAGGAAAAGAACGAGTCAATACGATACTTC  
ACTCAGGCTTGATTGATTAAAAAAATAACCGTATTGATGGTCTTGATT  
GATGAAGTTATGCTAACTATTATTAAAGCAAGAAGGAA

(SEQ ID NO: 152)

MLTHKNILLTIIFGLFMIILSACGMSNKEMAGIDNWEHYQKEKKITIGFDNTFV  
PMGFESRSGDYTGFDIDLNAVKEYGISVKWQPINWDMKETELNNGNIDL  
25 WNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKKLGAQSG  
SSGFDAFNAPDILKKFVKKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANY  
YLKQEG

30 Sequence description

A] Length: 649 bp - 216 aa (partial sequence)

35 B] TTG start codon is preceded by a possible  
typical Shine-Dalgarno sequence. Has a  
leader peptide

40 ID-154

Clone 2-c100

(SEQ ID NO: 153)

ATGAAAATTGGAAAAAAATAACCTTAATGTTTCTGCAATTATTTAACA  
ACAGTAATTGCATTGGGAGTCTATGTTGCCTCAGCTTATAATTTCGACTA  
ATGAATTGTCTAACAGACTTT

5

(SEQ ID NO: 154)

MKIWKKITLMFSAIILTVIALGVYVASAYNFSTNLSKTF

10 Sequence description

A] Length: 123 bp - 41 aa (partial sequence)

15

B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Has a  
typical leader peptide

20 ID-155

~

Clone 2-c1

(SEQ ID NO: 155)

25

ATGAAAAAAACAAAGACTATTACTGCTTTGGAGGCTTATTAATAATGATA  
ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAAA  
GGAATACCAGGCAGAACAGAACATTAAAGTCATACTTAAATATATATCAG  
ATAAAAATAACTATTTAGATAATATAAAAGTTATTACTTTCTATAAGTA  
TTTCTAAAGATGTACAAGATAAAAGTCAGTGAAACAAACACTGTTCATATA  
GACTAGAAAAGCAAAAGAACATCAAGAGTTCATTGGTAATTTGAACATGAA  
30 GTTAGTGAATCTAGTCAATATTCAACCGAAGTTAAAATCAAATACAGTAT  
CCAATCCAGTATAAAGATAATTCAATTGTTACTGAAAAAACACCGTCA  
GAACGTTATGATGAGTTGTTAGTTCAATTGATTCTCATTATTAAAAAA  
AATATAAAATATGATTACTTACTAAAACATCCGAAACTGAATTAAAAA  
GGTGTTCCTATAAGATTCCCTATAAAATTCTGAAATTGTAGCCCCTTTATAA  
35 ATCAATTAAATATAAAAAATCCTAAAAAATCATCTATTGCGTTACAAAAA  
CGGAAAGTAAAGAACATTATACAAATCAGTATTGATACTGATTCTGAGA  
TATATTCTATATTGAAGGTATTCA

(SEQ ID NO: 156)

40

MKKQRLLLLFGGLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYFKYISDKN  
NYLDNIKVYYFSISISKDVQDKVSETTCSYRLEKQKNQEFIGNFEHEVSESSQ  
YSTEVKNQIQYPIQYKDNSIRFTEKPSERYDEFVFSSFDSSLKKYKIYDYL  
HPETELKGVSYKIPINSEIVAPFINQLNIKNPKKSSISVTKTESKEYYYTISID  
TDS  
EIYSIFEGIH

Sequence description

5

A] Length: 687 bp - 229 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Has a  
typical leader peptide. C-terminus has yet to be  
verified

10

ID-156

15

Clone 2-c5

(SEQ ID NO: 157)

ATGACATTGACACCATTGATCAATTAGCGGTTAATACAGTCCGCACGCTT  
TCTATTGATGCTATCCAAGCAGCAAATTCTGGGCACCCAGGTCTTCCTATG  
20 GGAGCTGCGCCTATGGCTTATGTGCTTGGAAATAAATTCTTAAATGTAAAC  
CCA AAAAACAAGTCGCAATTGGACAAACCGTGACCGTTGTACTTCAGCT  
GGGCATGGTTCAGCTCTTATAGCCTACTTCATTAGCTGGCTATGATT  
TATCAATTGATGATT

25

(SEQ ID NO: 158)

MTFDTIDQLAVNTVRTLSIDAIQQAANSHPGLPMGAAPMAYVLWNKFLNVNP  
KTSRNWTNRDRFVLSAGHGSALLYSLLLAGYDLSIDD

30

Sequence description

35

A] Length: 272 bp - 90 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. No obvious  
leader peptide

ID-157

40

Clone 2-c8

(SEQ ID NO: 159)

ATGAGAACACTATTAGAATGATATTGCTATTCAAAGTTATCTTAGA  
TTGATTGGAATATCATTGGGAATATTCAAGACAGTCTTGTATTGCG  
ATTATTATTGGCTTGTATTACTATGCGAATCACAGTCAATCAGAATTG  
5 CTAATCAACTTAGTGACATTATTAGACAGGAAAAACATTTT

(SEQ ID NO: 160)

MRTLFRMIFAIPKFIFRLIWNIIWGIFKTVLVIAILFGLYYYANHSQSEFANQLS  
DIIQTGKTF

10

Sequence description

15

A] Length: 197 bp - 65 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

20

ID-158

Clone 2-c9

25

(SEQ ID NO: 161)

ATGTCAAAAAAAATAATATTAGGAATTTCATCTCTTATCTGTCGTTACTT  
TGGTGGCGTGTGGTTCATCAGACAAACAGCTACAAGATAAAGTTGAGAAA  
AAAGGGAAGTTAGTTAGCGGTGAGTCCAGATTATGCTCCCTTGAGTT

30

(SEQ ID NO: 162)

MSKKIILGILSLLSVVTLVACGSSDKQLQDKVEKKGKLVLAVSPDYAPFEF

Sequence description

35

A] Length: 153 bp - 51 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide (not in frame with nuc)

40

ID-159

Clone 2-c10

(SEQ ID NO: 163)

5 ATGAAAAAATCAAAGACTATTACTGCTTTGGAGGCTTATTAATAATGATA  
ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAAA  
GGAATACCAGGCAGAACAGAACATTAAAGTCATACTT

(SEQ ID NO: 164)

10 MKNQRLLLLFGGLLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYF

Sequence description

15

A] Length: 139 bp - 46 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

20

ID-160

Clone 2-c11

25

(SEQ ID NO: 165)

ATGATTGGAAAATTATATTATAGCTATAGAAAGTCACGCTTATTAAGAAGT  
ATTTTATGGCTTATTTAATTGTTGGGTATATATGTTAGGACAACGTGTTT  
TATTATCCACTGTTCCCTTATCACATCAAGAGATAAAACTAGCAGTAGATC  
30 AACATTTACTCAATAACTTTCAGCAGTAAGTGGTGGGAGTTAATAAAAT  
TAAATGTTTCACACTGGGGTTGAGTCCATGGATGTCAAGTATGATTATT  
GGAGATTGTTCCCTTATTTCGTGGGAAAAAATGCAACGAAGCGAAAAA  
GCAGAAGTAGCTCAATATACTTAATGCTTACTATCTCAGTTATAACAAGCA  
TATGGTGTTCAGGAAATCAATTATAAAAAGCTCTTATTAGGTTCTTATA  
35 GTGATATTGTTTT

(SEQ ID NO: 166)

MIGKLYYSYRKSRLRSILWLILIVGVYMLGQRVLLSTVPLSHQEIKLAVDQHL  
LNNFSAVSGGSFNKLNVFTLGLSPWMSSMIIWRFVSLFSWAKNATKRKAEV-A  
40 QYTLMLTISVIQAYGVSGNQFIKSSLGSYSDIVF

Sequence description

A] Length: 423 bp - 141 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
5 leader peptide

ID-161

10 Clone 2-c13

(SEQ ID NO: 167)

ATGAAAGGTCTATTGGATTTAGTTAATATTGCCAGAACGCCAGCTATT  
TTAGTCGCCTTGATAGCCATTATCGGTTAGTACTGCAGAAAAAAAGGTGTT  
15 CCTGATATTGTAAAAGGTGGAATAAAAACATTGTTGGCTTCTAGTGGTT  
TCTGAAGGTGCAGGGATAGTCCAAAATCCTTGAATCCATTGGAAAAATG  
TTTGAACATGCTTTCATTGGTGGGGTAGTCCTAATAATGAAGCCATT  
GTAGCAGTAGCTCTTACGAAGTATGGCTCAGCAACTGCTTGATTATGTTA  
GCAGGGAAATGATTAAATATTAAATTGCTCGTTACAAAAA

20

(SEQ ID NO: 168)

MKGLLDFLVNIARTPAILVALIAIIGLVLQKKGVVDIVKGGIKTFVGFVVSEG  
AGIVQNSLNPGKMFEHAFHLVGVVPNEAIVAVALTKYGSATALIMLAGMI  
FNILIARFTK

25

Sequence description

30

A] Length: 348 bp - 116 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
Shine-Dalgarno sequence. Possible leader  
peptide

35

ID-162

Clone 2-c21

40

(SEQ ID NO: 169)

TTGGTTGGTAAGCCCCAATTACTATTTAGATGAACCTACTTCCGGAATG  
GATACTTCCACACGTCAACGATTGGAAAGCTGGTTGCGACACTAAAAAA  
AGAAGGTGACACAATTGTCTATTCTAGTCATTATATCGAAGAGGTAGAAC  
ATACAGCTGATAGGATTTAGTACTTCATAAAGGAAAGTTATTACGCGATA

5 CAACCCCCTTGCATGAAGCAAGAAAAACCGAAAAGTTATTACCCGTT  
CCGCTTAGTTATCAAAAATTATTACCTACCTATTGATTACAGAGTGTGAA  
GCCAAGAGTGATAGTATAACGTTGTTACTGGGGAGGCTGAAACTGTATG  
GAAAATACTGGCAGATAATGGTTGTCCTATTGAAGCTATTGAGATGACCA  
ATAGAACCTTGTAAATCGTATTGAGACTACTAAGGAGGTAAAACATG  
AGAATCTTA

(SEQ ID NO: 170)

MVGKPQLLDEPTSGMDTSTRQRFWKLVATLKKEGDTIVYSSHYIEEVEHTA  
10 DRILVLHKGKLLRDTTPFAMKQEKTKEKLFTVPLSYQKLLPTYLITECEAKSDSI  
TFVTGEAETVWKILADNGCPIEAIEMTNRTLNRIFFTKEVKHENL

Sequence description

15

- A] Length: 462 bp - 155 aa (partial sequence)  
B] Putative TTG start codon is not preceded by  
an obvious Shine-Dalgarno sequence. No obvious  
20 leader peptide. N- and C- termini require further  
examination.

ID-163

25

Clone 2-c25

(SEQ ID NO: 171)

30 TTGAAAAAAATCCAAGAGAAGCCGTAAGGCAGTGACAACAAGTGGTGAGA  
AGACTTACTTGAGGATTGGCAAAATGAATTCTAGACGAAGTCATTA  
ATGTTATGGTTTATATACCTTGAATAAGACAAAATCTGCTAACTTAAATA  
AGGCCTATATCATGAAAGTTGCTAATGATTGCTTGCCTTCAGAATGTTATGA  
CGGCCGAAGATGCTGTGCTAAAATTCTGATTTTCAGATAAAAAGTAA  
GGACTAAAACAGAAACGAAGAAGAAACAATCGAATGTTCTGAATGGAGT  
35 AATCCTGATTATAAGATGAGGTTAGCCCAGAAAAAGAAATTGAATTAGA  
ACAGTTT

(SEQ ID NO: 172)

40 MKKSRSRKAVTTSGEKTLLEDLAKMNFLDEVINVMVLYTLNKTSAANLNK  
AYIMKVANDFAFQNVMTAEDAVALKIRDFSDQKVRTKTETKKQSNVPEWSN  
PDYKDEVSPEKEIELEQF

Sequence description

A] Length:360 bp - 120 aa (partial sequence)  
B] N- and C- termini require verification.

5

ID-164

Clone 2-c28

10 (SEQ ID NO: 173)  
ATGACGAATCATATTACTAAACTGATAGAAAATAGCGGAAAAAAATTGAC  
AGAAATTAGCGAAGCTACAGATATGCCTATCCTACACTTCTGGATACAA  
TCAAGGAATCCGCAAACCTAAAAAAAGATAATGCTGAAAAATTGGCAAAAT  
ACTTTAATGTTCCGTCGCTTACATTATGGGACTTGATAGCAACCCACATG  
15 CTCCATCAAATCTT

(SEQ ID NO: 174)

MTNHITKLIENSGKKLTEISEATDIA YPTLSGYNQGIRKPKDNAEKLAKYFNV  
SVAYIMGLDSNPHAPSNL

20

Sequence description

25 A] Length:218 bp - 72 aa (partial sequence)  
B] ATG start codon is preceded by an  
obvious Shine Dalgarno sequence. No obvious  
leader peptide.

30

ID-165

Clone 2-c29

35 (SEQ ID NO: 175)  
TTGATGAAAAGGAATAAACATTACCGTTAACAGAAACTACCTATTATATT  
TTATTAGCTTGTTGAGGAAGCGCATGGCTATGCTATTATGAAAAAAAGTT  
GAAGAAAATGAGTGGCGGTGATGTTAGAATAGCCGCAGGGACAATGTACGG  
TGCCATTGAAAATTACTAAACAAAAATGGATAAAGTCTATCTCAAGTGA  
40 CGATAGAAGAAGAAAAGTTATATTACTGAGACAGGAAAAGAAATAG  
TAGAACTTGAAACGAATCGATTAAGAAAGTTACTTAATACTGCTAATCAGT  
TGGGTTTGGAGGAGATGGTTATGATAAAGTT

(SEQ ID NO: 176)

MMKRNKHLPLTETTYYILLALFEEAHGYAIMKKVEEMSGGDVRIAAGTMYG  
AIENLLKQKWIKSISSDRRRKVYIITETGKEIVELETNRLRKLNTANQLGFG  
GDGYDKV

5

Sequence description

10 A] Length:337 bp - 112 aa (partial sequence)

B] TTG start codon is preceded by an  
obvious Shine Dalgarno sequence. Actual start  
codon may ATG that comes immediately after the  
TTG. Potential leader peptide.

15

ID-166

Clone 2-c35

20

(SEQ ID NO: 177)

CCCATTACTGGTGAGTTAATAGCTGAGAAATTAGGAGTACCAAGAGCAGC  
ACTAAGGTCTGATTGCGGGTTTAAGTATGCTAGGTATCATAGATGCAA  
ACCTAACGGTTGGTTATTTTATTAGGACAGTATCATGCTTCAATAGGGAC  
25 AAGTCATTTGAAAAGATGACAGTTTCAGAAATTATGGGGATCCTTCTGAC  
AGTTCATAAAAAGATTCAAGTTATGATGTTATTGTACATATTTTATGGA  
AGATGCTGGTTGTGCTTTATCTTGGATGATGATGATTCTCTGTGGAGTC  
GTGTCACGTAAAGATTACTAAAAACCACTATTGGCGGAGGAGATCTTCT  
30 AAAATGCCAATAGGAATGGTGATGACACGTATGCCACACGTGACAACGT  
TTTAGAAAATGAAAGTCTTTGCGGCAGCTGATAAAATTAGTGAGCAGAA  
AAGTGGATAGTCTCCCTGTCGTCATGATAAGCAATATCCGAAAAAT  
TTA

(SEQ ID NO: 178)

35

PITGELIAEKLGVPRALARSDLRVLSMLGIIDAKPKVGYFYLQYHASIGTS  
HF EKMTVSEIMGILLTVHQKDSVYDVIVHIFMEDAGCAFILDDDFLCGVVS  
RKD LLKTSIGGGDLSKMPIGMVMTRMPHVTTVLENESLFAAADKLVS  
RKVDSLVR VRHDKQYPEKF

40

Sequence description

A] Length:511 bp - 170 aa (partial sequence)

B] N- and C-termini to be determined

5 ID-167

Clone 2-44

(SEQ ID NO: 179)

TTGGAAGTCATCATGCAATTATTATAGTATTATTGGTATTTATTGGTAT  
TAGGAATTGTGTATGCAATTCTTCAATCGTAAGAGTGTTCTCTAAGTT  
AATTGGAAAAGCTCTTATCGTTCAATTCAATTGCGCTAATCTTAGTACGT  
ATCCCACTAGGCCAACAAAGTTGTTAGTGTGTTCAACTGGAGTTACTAAA  
GTAATCAACTGTGGTCAAGCTGGTT

15 (SEQ ID NO: 180)

MEVIMQFIYIIGILLVLGIVYAIISNRKSVSLSLIGKALIVQFIIALILVRIPLGQQ  
VVSVVSTGVTKVINCGQAG

20 Sequence description

A] Length:233 bp - 77 aa (partial sequence)

B] TTG start codon is preceded by a

25 possible Shine Dalgarno sequence. Actual start codon may occur further downstream. Potential leader peptide.

30 ID-168

Clone 2-46

(SEQ ID NO: 181)

35 CAACCTAATAAGCTTAGAAAGTGTGAGATTGATATTAATGCTTCCAG  
CATTATAATTACTAACCAATTGGAATAAGCAAATAAGACCAATCTGTT  
TCCGTTGCTGAGACATACTTACTTCCTTAGATTATACTCTGGTACTAAGA  
ACGGTAAAGGTAAATACCAACAGTTCTGAAATTCCAAATAAGCAACT  
ATTACTATCCAAACGATGCAGTTAACGAAAGTCGCTCTACTGTTA  
40 CAATCAGCAGGCTGCTAAATTGAAAGTATCAGGTGATACATTAGCAAC  
AATGTCAGATGTTCTCAATCCTAAATCTTAGATT

(SEQ ID NO: 182)

QPNKALESDEIDINAFAQHYNLTWNKANKTNLVSAETYFTSFRLYSGTKN  
GKGKYQTVSEIPNKATITIPNDAVNESRSLYLLQSAGLLKLKVSGDTLATMSD  
VVSNPKSLD

5

## Sequence description

10 A] Length:344 bp - 114 aa (partial sequence)  
B] N- and C- termini require verification

ID-169

15

## Clone 2-47

(SEQ ID NO: 183)

20 ATGAAATGTATAATAAATAATATAAAAATAAAATGATAATTGAGAT  
TTATCATAGAAGGAAAACCTATTTGAAATTAAAATAAAATCATATTATCTAC  
TGCAGCTCTTACTGCTCTTTAGGATATAATAGCGTTACTGCGGATACA  
TATAATAACTATCAGCCACATAGATCAAATAATATGGATTAACTGAGGA  
ATATAACTATAATAACCAGATAGAACCTCAGGAGCGTATAAAAAACCTAA  
25 ATATAACCTTT

(SEQ ID NO: 184)

MKCINNINKIKMIEIYHRRKTILKLNKIILSTAALTALFLGYNSTADTNNY  
QPHRSNNMDLTEEYNYNQIELQERIKNLNIPF

30

## Sequence description

35            A] Length:264 bp - 88 aa (partial sequence)  
B] There is a Shine-Dalgarno sequence upstream  
of this sequence. Potential leader peptide  
sequence

40

ID-170

Clone RS-58b

(SEQ ID NO: 185)

TTGGGTGATTATTATGGTAAGAAATATTTGGT GAGGCAGCTAAAAAAGA  
CGTCGAACATATGGCTAAGAAAATCATTAAATGTCTATAAAACACGGTTAA  
AAAACAACACTTGGTTATCAGAAAATACAAAAGCAATGGCCATTAAGAAA  
5 CTTGATAACATGAGATTAATGATTGGCTATCCAGAAGATTATCCTGATCTT  
TATCGTCAGTACCAATTGATAGTAAAGCAAGCTTCTTGAAAACAATGAT  
AACTACAGAAAATTATCGAACAGAAAACATTGAAGAATTAAACCAGTC  
TAATCAACGTGAACATTGGCAAATGAGTGCCAATGCTGTAAATGCTTATAA  
10 TGATCCTAATACCAATTCCATAGTCTTCCAGCAGCGATTTCAATCACCA  
CTGTACGATAAAACTAAAACAGTTAGTCAAAATTATGGAGCTATCGGAGC  
AATTATTGGTCATGAAATTTCACACTCATTGATATTAAATGGTATGAAATA  
TGACGAGAAAGGGAATCTTCACGATTGGTGGACTAAAGAAGATTAAATC  
ATTATAAGAAATCAACACAAAGCTATGATTGACCAATGGGATGGCCTTAAA  
15 GCAGATGGCGGTAAAGTTGATGGTAAATTAACTTAGCAGAAAATATTGC  
AGATAATGGTGGTGTATGGCATCTCTAGAACGCTCTAACAGACTGAAAAAAAT  
CCAAACTATAAAGAATTGGTAAATCATGGCAAGTATTGGCGTAAAAAA  
GCAACCAAAGAACAAAGTAAGTCCTCAATTCAAGTCAGATGTTCATGCACC  
ATATGAATTGAGAGCTAACATCCCAGTACGTAATTCCAAGAATTGATGAA  
20 TGCCTTGGTGTAAAAAAGGCGATTCAATGTATCTAAAACCAGAAAAAC  
GTTTGACACTTGGTAA

(SEQ ID NO: 186)

MGDYYGKKYFGEAKKDVEHMAKKIINVYKTRLKNNTWLSENTKAMAIKK  
LDNMRLMIGYPDYPDLYRQYQFD SKASFFENNDNYRKLSNKKTFEEFNQSNQ  
25 REHWQMSANAVNA YNDPNTNSIVFPAAIFQSPLYDKTKTVSQNYGAIGAIIGH  
EISHSF DINGMKYDEKGNLHDWWT KEDLNHYKKSTQAMIDQWDGLKADGG  
KVDGKLTLAENIADNGGVMASLEALKTEKIQTICKFLNHGQVFGVKKQPKNK  
VSPQFSQMFMHHMN\*

30 Sequence description:

A] Length: 819 bp - 272 aa (full length gene)  
(107 bp of additional DNA sequence (> onwards) is  
also included. While not in-frame with the  
described orf, it also shares strong homology  
with the neutral peptidases.  
35 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-89 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-89 gene sequence.  
ID-89 and ID-170 together show homology over their combined entire length  
40 with the neutral endopeptidases from Lactococcus and Lactobacillus. Possesses  
TTG (possible ATG start codon located 13 bp further downstream) start  
codon with no obvious signal peptide. Shine Dalgarno sequence not  
immediately obvious. Possibly located further downstream

ID-171

5 Clone 2-18/22b (Mod2)

(SEQ ID NO: 187)

ATGACCATGATTACGCCAAGCTTCATTAAGGTATCTCTAGATGAAACAAAT  
CGTATGATGCGTATGATATCAGATTATTAAGTTATCGCGCATTGATAAT  
10 GAAGTAACGCATTAGATGTTGAAATGACGAATTACAGCTTCATGACC  
TCAATTGAAATCGATTGATCAGATTAGAAATCAAAAAACAGTCACAGG  
AAAAGTTATGAAATTGTCAGAGATTATCCTCTTAAGTCAATTGGGTGGA  
AATTGATACAGATAAGATGACTCAAGTGATTGATAACATTAAATAATGC  
15 AGTCAAGTATTACCAAGATGGTGGTAAGATTACAGTTAATCTACGCACAAC  
TAAAACGCAGATGATTATCAATATCAGACCAAGGCTAGGTATTCCCAA  
AAAAGATTACCTCTCATTTGATCGTTTATCGTGTGATAAGGCGAGA  
AGTCGTCAACAGGGTGGGACTGGACTTGGTTGTCAATTGCAAAAGAAAT  
TGTAAAGCAGCATAAGGGATTATTGGGCTAAGAGTGAGTATGGTAAAG  
20 GGTCTACTTTACAATCGTCTGCCTATGATAAAAGATGCTGTAACATTATGA  
AGAATGGGAGGACGTTGAAGATTAA

(SEQ ID NO: 188)

MTMITPSFIKVSLDETNRMMRMISDLLSLSRIDNEVTHLDVEMTNFTAFMTSIL  
NRFDQIRNQKTVTGKVYEIVRDYPLKSIWVEIDTDKMTQVIDNILNNAVKYSP  
25 DGGKITVNLRRTKTQMILSISDQGLGIPKKDLPLIFDRFYRVDKARSRQQGGTG  
LGLSIAKEIVKQHKGFIWAKSEYKGSTFTIVLPYDKDAVTYEEWEDVED\*

Sequence description:

30 A] Length: 613 bp - 212 aa (full-length gene possibly)  
B] Possible Shine Dalgarno sequence present  
upstream of a ATG start codon. May not have yet  
determined the N- portion of this gene. No  
35 obvious signal peptide.

ID-172

40 Clone 2-54balternate (107b)

(SEQ ID NO: 189)

TTGAAAAAAATTATTACTTCTATTCTATTACTTAGTTGCATTTTTATGC  
CAACCATCTGCTGAATCTTTAATGCTTCCGCTAACACATGCCTAGCAGT

TGATTAGATTCAAGGAAAAATCTTGTATGAAAAAGATGCTAACAAACCCG  
CTGCTATTGCTTCCTTGACTAAAATAATGACCGTTATATGGTCTATAAAG  
AAATTGATAACGGTAACCTCAAGTGGAAATACCAAAGTAAATATATCTGAC  
5 TACCCTTATCAACTAACACACCGAATCTGATGCTAGTAATGTTCCCTTAGAA  
AAAAGGCCTATACTGTTAAACAACCGTGGACGCCATGATTCTAGT  
GCTAACAGTGCAGCCATTGCTTAGCTGAACATATTCAGGAACGTGAAAGT  
AAATTGTTGATAAAATGACTGCTCAATTGGAAAAGTGGGGAAATCATGAT  
AGCCACCTAGTCAATGCTCTGGCTAAATAATAGTATGTTAGGCAATCAC  
10 ATTTATCCAAAATCGTCACAAAACGACGAAAATAATGAGTGCACGTGA  
TATTGCTATTGCTGCCTACCATTGGTCAACGAATATCCTCCATTCTTAAG  
ATTACTAGTAAGTCCGTTGCTAAATTGATAAAAGATATTATGCATTCTTAT  
AACTACATGCTACCAGATATGCCTGTCTTAGACCAGGTATTACAGGTTG  
15 AAAACTGGGACAACGGAATTAGCTGGCCAATCTTATTGCTACATCTACT  
GAAAGTGGAAATGAGACTACTCACTGTTATTATGCATGCTGATAAGGCCAT  
AAAGACAAATATGCTCGCTTACAGCAACTAACTCTCTTGAACATATAC  
ACAAACACCTACGAACCTAACCTGTATTAGCTAAAGGAGCTGCATATAA  
AGGTAAAGAAGCAAGTGTGAGAGACGGAAAAGAACAAATCGGTATCGCT  
20 GTGCTAAAAACGATTGAAAGTAGTACAGAAGAAAAATATCACTAAACA  
AAATCAGTTAAAATTAACTTAAAAAGAGCTTACTGCTCCTATTACAAA  
AAAAGAGAACCTAGGGAAAGCTTATTACGTTGACCTTAATAAGGTTGGAA  
AAGGCTATCTCATAAAGGAACCTAGCGTTCAATTAGTGGCAAAAGATAGT  
ATTGAGCGCAGTTCTCCTCAAAGTGTGGTGGAAATCATTGTGCGCTAC  
GTTAACGAAAAACTTAA

25 (SEQ ID NO: 190)  
MKKIITSILLSCIFFMPTISAESFNASAKHALAVDLSGKILYEKDANKPAAIA  
SLTKIMTVYMVYKEIDNGNLKWNTKVNISDYPYQLTRESDASNVPLEKRRYT  
VKQLVDAAMISSANSAAIALAEHISGETSKFVDKMTAQLEKWIHDHSHLVNA  
SGLNNNSMLGNHIYPKSSQNDENKMSARDIAIAAYHLVNEYPSILKITSKSVAKF  
30 DKDIMHSNYMLPDMPVFRPGITGLKTGTTLAGQSFATSTESGMRLLTIVM  
HADKADKDKYARFTATNSLLNYITNTYEPNLVLAKGAAYKGKEASVRDGKE  
QSVIAVAKNDLKVVQKKNITKQNQLKINFKELTAPITKKENLGKAYYVDLN  
KVGKGYLIKEPSVHLVAKDSIERSFFLKVWWNHFVRYVNEKL\*

35 Sequence description:  
A] Length: 1236 bp - 412 aa (full-length gene sequence possibly)  
B] A possible Shine-Dalgarno sequence precedes the putative 'TTG' start codon. (needs further cloning and sequencing to verify N-terminus)

40

ID-173

Clone 3-60b

(SEQ ID NO: 191)

ATGACGCTTCGAGAATTAACAATAGAAGAACATTAAAGAACATTCAAGGAAA  
5 TTATGATTACAATCATTTCACAAACACCTGAGATGGCTAAACTTTAGA  
AAAACGCGCTATGATGTTAGGTATTGGGATATCAAGTAGAAAATAAAC  
TAGAGATAATCAGTTATCTTATATTATGCCAGTCACTGGTGGTTCAAAT  
GAAAATTGATTCAAGGACCAGTCATTCAAATTCTAAGTATCTAAAACAATT  
10 TTATAAAGCATTGCAAGGCTATGCCAAATCCAACGGTGTCTAGAATTAAAT  
AGTTGAGCCTTGATGATTACCAATTATTCACTAGTCGGGAGTCCTAGT  
AATCAGGGAAATGATAATCTGATTGAAGATTACCAAGTTTCAGGTTATCAC  
CATGATGGTTAACAACTGGTTACTGGTAAATATTATCTTGGCACTATG  
15 TTAAAAATTAGAAGGTGTCATTCTGAAACGTTACTATCTTCATTCTCTAA  
GACAGGACGAGCTTGGTTAAGAAAGCAATGTCTTGGAATCAAGGTTC  
GCGTTCTAACGTGATGAGCTACATTATTAAAGAGATAACAACTTCTA  
CGTCAAATAGACGTGATTATATGGATAAGTCCTTAGATTATTATCAAGATT  
TTTACGATAGCTTGAAGGCAAGGCTGAATTGTGATTGCCACTTAAATT  
20 TTAGAGAATACGACCATAACTGCAAATAAGCTGAAGCATTGGAAAAT  
AAGCTT

20

(SEQ ID NO: 192)

MTLRELTIEEFKEHSGNYDSQSFLQTPEMAKLLEKRGYDVRYLGYQVENKLEI  
ISLSYIMPVTGGFQMKIDSGPVHSNSKYLQFYKALQGYAKSNGVLELIVEPF  
25 DDYQLFTSSGVPSNQGNDNLIEDFTSSGYHHDGLTTGFTGKYLSWHYVKNLE  
GVTSETLLSSFSKTGRALVKKAMSGIKVRLKRDELHLFKEITTSTSNNRDY  
MDKSLDYYQDFYDSFEGKAEFVIATLNFRDYHNLQIKAEALENKL

Sequence description

30

A) Length: 771 bp - 257 aa (partial gene sequence)

25

B) This gene sequence was not identified using the LEEP system. It was identified immediately downstream of the ID-65 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-65 gene sequence. Sequence Characteristics:

35

No obvious leader peptide sequence  
Orf is preceded by a potential Shine-Dalgarno sequence.

40

ID-174

Clone 2-17b (ID-80b)

(SEQ ID NO: 193)

TTGTCATTAAGTTGGTGCAGTGTAAATCTTATCCCTCCTAAAATCATGG  
GATCAGTTATTGATGCTATTACAACGGAAAAATTAAACAAGACCACAATTAC  
TATGGAATTATTAGGTTGGTTGTCAAGCTTAGCTATGTATGGGCTGCG  
5 TTATATTGGCGTATGTATTTAGGGACTTACAATTAGGCCAAGTT  
GTCAGATAACGTTATTGAACATTACAAAAATGTCTCCTCTTTATC  
AGAAATATCGTACAGGTGATTAATGGCGCACGCGACCAACGACATCAAT  
TCTCTAACACGTCTGCAGGAGGAGTTATGTCAGCAGTGGATGCCTCT  
ATCACAGCATTAGTAACGCTTATCACCATGTTACTATTCGTGGCAA  
10 ATGACATTAATTGCGGTTATCCCTTGCCCTTAATGGCCTAGCACTAGTA  
AATTGGGGCGAAAAACCCATGAAACCTTCAAAGAATCTCAGGCAGCCCTT  
TTCAGAATTAAATAATAAGTG

(SEQ ID NO: 194)

MSLSLVAVLNLI<sup>P</sup>KIMGSVIDAITGKLTRPQLLWNLLGLVLSALAMYGLRYI  
15 WRMYILGTSYKLGQVVRYRLFEHFTKMSPSFYQKYRTGDLMAHATNDINSLT  
RLAGGGVMSAVDASITALVTLITMFFTISWQMTLIAVIPLPLMALVNWGEK  
PMKPSKNLRQPFSELNNKV

20 Sequence description

A) Length: 534 bp - 178 aa (partial gene sequence)

B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-80 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-80 gene sequence.

25 Sequence Characteristics:

No obvious leader peptide sequence

Orf is preceded by a potential Shine-Dalgarno sequence.

30

ID-175

Clone 2-11Ab (ID-103b)

35 (SEQ ID NO: 195)

ATGCATATTGAGACTGTTATTGATTCAAAGAATTAGGAAAAAGATATCGT  
TTAAAAAAATCCTACAAAAGAATTAAATAGCTGATACTTAGAACAAAGTCTTA  
GAAGTGATAAAAAGAAGTTGATTATTATCAATCTCAAAATTATTATGTTGTT  
40 GGTTATTATCTTATGAAGCATCTGCTGCTTGTACACATTAAAGTT  
CTCAACAGAAGTTGGCTGGAGAACATCTAGCTTACAGTACATAAAG  
ATTGTGAGAACGAAGCTTCTTAAGTTATGAAAATGTTAGATTAGCAG  
ATAATTGGACTGCTAATGTTCTGAGCAAGAACATCAAGAGGCAATTGCTA

ATATTAAAGGACAAATTAGACAAGGAAACTTATCAAGTAAATTATA  
CTAGAGCTTAGCCAACAATTATGCTCGGATCC

(SEQ ID NO: 196)

5 MHIETVIDFKELGKRYRFKNPTKELIADTLEQVLEVIKEVDYYQSQNYVVGY  
LSYEASAAFD SHFKVSQQKLAGEHLAYFTVHKDCENEAFPLSYENVRLADNW  
TANVSEQEYQEAIANIKGQIRQGNTYQVN YTLELSQQLCSD

10 Sequence description:

A] Length: 440 bp - 146 aa (partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was  
15 identified downstream of the ID-103 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-103 gene sequence.  
Shine Dalgarno sequence present upstream of  
ATG start codon, No apparent leader peptide sequence

20 ID-176

Clone 2-18/22b(b) (ID-104b)

(SEQ ID NO: 197)

25 GTGAATAATATGTTTATCTAAAATAGCCTGGCATAATTAAAACATTCT  
ATAGACCAGTACATACCATT CCTCTTAGCCAGTTATTACTTATT CATTGA  
CTTGTCTACGCTACTAATCTTAATGAGTGCTGTTGGAAAGAGATATGGGA  
CAGCGGCAACGGTCTTTCTTGGAGTGATTGTTGTCAATCTTGC GGT  
AGTCATGGAACATTATAGCTACAATATCTTGATGAAACAGCGTAGTAGTG  
30 AATTGGACTGTATAACATTTGGGGATGAATAAACGTCAAGTTGCGCGTG  
TAGCTAGTCTAGAGCTGTTATTATTTATATTTCTTCTATAGGAAG  
TCTGTTAGTGCTTTTGCTAAATTATTTAATTGTTGTCAACATTA  
TTAACTATCATGCACTAAATCTTAGTTAAGTTATGGCCATTATTATTG  
TATCGTTATATTACAGGTATTTCTGACTTAGAAGTTCCAGTTATCGA  
35 CATGTTCATTTATCATCCCCATTAAGTCTTTAGAAAAGAAAACAACAGGG  
GAAAAAGAACCAAAAGGTAATCTTATACTTGCAATTAGCGTTAGTAGCT  
ATGCCATCGCTTATACAATGGCTTACTTCAGGTAAAGCACCTGCATTA  
GCTGTTATCTATCGTTCTTGCAGTACTTTAGTAATTGCTGGTACTT  
ATCTTTTATATTAGTTATGACATGGTACTAAAAAGGTTGCGTCAAAA  
40 CAAGCATTATTATAAAATCTGAGCATTGTATCAACTTCGCAAATGAT  
TTTCGAATGAAGCAAAATGCAGTAGGGTTAGCAAGTATCACTTATTAGC  
TGTTATGGCTCTAGTTACTATTGCTACAACAGTCTCACTCTATTCAAATACA  
CAAAATGTTGTTACCGGACTATTCCAAAATCAGTAAGTTATCAATAGAT  
AATTCAAAAGGTGACGCGAAAAATATATTGAAGAAAAGATTGAAAGAA

ACTAGGTAAGTCATCTAAGGAAGCTATCACTTATAATCAGACAATGATTTC  
GATGCCAGTTAGTCAATCAAGTGACTTAATATCACATCTA

(SEQ ID NO: 198)

5 MNNMFYLKIAWHNLKHSIDQYIPFLLASLLLSTCSTLLILMSAVGRDMGTA  
ATVLFLGVIVLISIFAVVMEHYSYNILMKQRSSEFGLYNILGMNKRQVARVASL  
ELFIYYIFLISIGSLFSAFFAKFIYLIFVNIINYHALNLSLSLWPFIICIVIFTGIFLTLE  
VPVIRHVHLSSPLSLFRKKQQGEKEPKGNLILAILALVAIAIAYTMALTSKGAP  
10 ALAVIYRFFFAVLLVIAGTYLFYISFMTWYLKRLRQNKHYYYKSEHFVSTSQM  
IFRMKQNAVGLASITLLAVMALVTIATTVSLYSNTQNVVTGLFPKSVSLSIDNS  
KGDAKNIFEKILKKLGSSKEITYNQTMISMPVSQSSDLISHL

Sequence description:

15 A] Length: 1119 bp - 373 aa (partial gene sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified upstream of the ID-104 gene which was identified by LEEP, during  
cloning and sequence analysis of the full-length ID-104 gene sequence.  
20 Possible Shine Dalgarno sequence present  
upstream of a GTG start codon. Possesses a potential  
leader peptide sequence

25 ID-177

Clone 2-5b (ID-112b)

(SEQ ID NO: 199)

30 ATGGTTGAGCCAATTATTCATAACAGGACTTCATAAAAGTTTGGGAAA  
AATGAGGTTTAAAAGGCATTGACTTGGATATTCAAGGAGAACGTGGT  
GGTTATTATTGCCCTCTGGCTCTGGTAAGTCAACATTAAAGAACAAAT  
GAATCTCTTGGAAAGTACCAACAAAGGGAACAGTGACTTTGAAGGGATTG  
ATATAACAGACAAAAAGAATGATATTAAATGCGCGAAAAAATGGGC  
35 ATGGTTTTCAACAGTTCAATCTATTCCAAATATGACTGTACTAGAAAAT  
ATTACTTATCACCTATTAAGACAAAGGGACTTCTAAGCTTGTGCTCAG  
ACAAAAAGCATACGAGCTACTGAAAAAGTTGGACTCAAAGAGAACGGCTAA  
TGCTTATCCAGCAAGCTTATCTGGAGGACAACAACACGGATTGCTATTGC  
AAGAGGGCTTGCAATGAATCCTGATGTCCTTCTTGTGAAACCTACFTCA  
40 GCTCTTGATCCTGAAATGGTAGGTGAAGTCTGACTGTTATGCAAGATTAA  
GCTAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTGCA  
CGTGAAGTAGCGGATCGTGTCAATTtTATGGATGCAGGGATTATTGTTGAG  
CAAGGGACCCCTAAGAAAGTATTGAGCAGACAAAAGAAATCCGCACAAG  
AGACTTCTTAAGTAAAGTATTATAA

(SEQ ID NO: 200)

MVEPIISIQGLHKSGKNEVLKGIDLDIHQGEVVVIIGPSGSGKSTFLRTMNLLE  
VPTKGTVTFEGIDITDKNDIFKMREKMGVMFQQFNLPNMTVLENITLSPIKT  
5 KGLSKLDAQTKAAYELLEKVGKKEKANAYPASLSGGQQQRRIAIARGLAMNPDV  
LLFDEPTSALDPEMVGEVLTVMQDLAKSGMTMVIVTHEMGFAREVADRVIF  
MDAGIIVEQGTPKKVFEQTKEIRTRDFLSKVL\*

10 Sequence description:

A] Length: 735 bp - 244 aa (full length gene)

B] This gene sequence was not identified using the LEEP system. It was  
15 identified downstream of the ID-112 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-112 gene sequence.  
Shine-Dalgarno sequence precedes the 'ATG'  
start codon. No obvious leader peptide

20 ID-178

Clone 2-5c (ID-112c)

(SEQ ID NO: 201)

25 ATGTCTCA~~s~~TATCAAGAGTGTTAGAAAACGACTCACTCGTAAAGATATT  
AAGTCAGATTAGAACGCTATTAAAGGAGATGAATCTGAAATTCAAGGATCG  
TTTTACAAAACATTAGAACATTGGAACGGCGGGATTGAGAGGTAAACTTG  
GAGCAGGAACCAATCGTATGAATACTTATATGGTGGGGAAAGCAGCACAA  
30 GCATTAGCTAATCGATTATTGATCATGCCCTGAAGCTATTGCACGTGGAA  
TTGCAGTTAGTTATGATGTCCCCTATCAATCTAAGGAATTGCAGAATTA  
ACTTGGTCCATTATGGCAGCAAATGGTATTAAAGCCTTATATTAA

(SEQ ID NO: 202)

35 MSHMNYKEIYQEWELENDLGD~~K~~DIKSDLEAIKGDESEI~~Q~~DRFYKTLEFGTAGLR  
GKLGAGTNRMNTYMVGKAAQALANRLLIMALKLLHVELQLVMMMSRYQSKE  
FAELTW~~S~~IMAANGIKALYL

40 Sequence description:

A] Length: 366 bp - 122 aa (partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-112 gene which was identified by LEEP,

during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence preceded the 'ATG' start codon. No obvious potential leader peptide sequence.

5

ID-179

Clone 2-5d (ID-112d)

10 (SEQ ID NO: 203)  
ATGCAACCTGTAAAAGTCGATGAACCTTCTGTTGAAGAAACCATTACTATT  
TTGAAAGGTATCCAAAAAAAATACGAAGATTATCATCACGTAAAATATAA  
TAATGATGCCATAGAACAGCTGCAGTACTATCTAATCGTTATATCCAAGA  
CCGCTTTTACCTGATAAAGCAATAGACTTATTAGATGAAGCTGGTTCTAA  
15 AATGAACCTAACACTAAATTGTTGATCCAAAAGAAATTGATCAACGTCT  
CATTGAAGCAGAAAATTAAAAGCGCAAGCGACTCGTGAAGAAGATTACG  
AACGTGCAGCTTACTTCCGTGACCAGATTGCAAAATATAAAGAAATGCAG  
CAACAAAAGGTGACGATCAAGATAACACCTATTATTACCGAAAAACAAT  
TGAGCACATCATTGAAGAAAAACGAATATCCCTGTTGGTATTAAAAG  
20 AAAAAGAACAACTCAATTAAATTAAATCTCGCAGATGACTTGAAACAGCAT  
GTGATCGGCCAGGATGACGCTGTCATTAAGATTGCAAAAGCTATTGTCGT  
AATCGAGTTGGTCTTGGTAGCCCCAACCGTCCTATTGGTCTTTATTG  
TAGGACCAACCAGGTTGGTAAAAGTAACTGAACCTTCTAAACAACTAGCAATTG  
AGCTCTTGGTTCAGCTGATAGTATGATTGCTTTGATATGTCAGAGTACAT  
25 GGAAAAGCATGCTGTTGCTAAATTAGTCGGAGCGCCTCCAGGATACGTGG  
GATACGAGGAAGCTGGACAACACTAACTGAAAAGGTTGTCGAAATCCTTAC  
TCGCTCATCCTCTAGATGAAATTGAAAAAGCTCATCCGATGTCATGCAT  
ATGTTCTTGCAGGTCTTGATGACGGTCGATTAACAGATGGACAAGGAAG  
AACTGTTAGTTAAAGATACCATTATCATGACCTCAAATGCTGGTTC  
30 TGGTAAAAGTGAAGCAAGTGTGGCTTGGCCTCACGAGAAGGTAGGA  
CGAATTGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCAT  
GCAAGC

(SEQ ID NO: 204)  
35 MQPVKVDEPSVEETITILKGIQKKYEDYHHVKYNNDIAIEAAAVLSNRYIQDRF  
LPDKAIDLLEAGSKMNLTLNFVDPKEIDQRLIEAENLKAQATREEDYERAAY  
FRDQIAKYKEMQQKVDDQDTPITEKTIEHIIIEKTNIPVGDLKEKEQLSQLINL  
ADDLKQHVIGQDDAVIKIAKIRRNVRGLSPNRPIGSFLFVGPTVGKTELSK  
40 QLAIELFGSADSMIRFDNSEYMEKHAVAKLVGAPPGYVGYEEAGQLTEKVRR  
NPYSLILLDEIEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDTIIMTSNAGS  
GKTEASVFGASREGRTNSSVPGDPLESTCRHAS

Sequence description:

A] Length: 1070 bp &gt; 356 aa (Partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-112 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence preceded the 'ATG' start codon. No obvious potential leader peptide sequence.

10

ID-180

Clone 2-7b (ID-113b)

15

(SEQ ID NO: 205)

ATGAGAGGGAAGGTTATTACGGCACAAACCCTATAGGTCTTTCTATTCTTCTATTTCATTGGATTCTAACATCGAGAGAATACATCATC  
ATCGTATAAAGCAGGTAGATGCGAAGAGTGATTAACAGGATTAAAACC  
CATTGCCATTATCAGCATTGATACAAAGCAACAAGTTATTCCCTCTGTT  
ACAAAAGAAGGCGGAAAATATGTCAGGCTAGGGATAATATTAATGTTGA  
TATCGAATTACGGGATTCTCCAAGTAGATCACATCATTATCAGAAAAGCC  
GAGAATTAGGACAAAAGGTTAATATCATATAGAGGAAATTCCCTCTCGTT  
ACTTGATAAGAAGTCATTGAAAGTTAAGTTGTTACTAATAAGTTAAAGG  
AAAAGAAGCATCGATTAGCAGGAATGCCTAAAGAATCGGAGTGGGTATTG  
CATGGTCCCTTCTAGACAGAACATTATTAAGAAATTATCTGAGTTATAAT  
ATTGCTGGTGAGATTATGCCTATGCCCAAACGTTCGCTACTGTGAGTTAT  
TTGTCAATGGTGAGTATCAGGGAG

20

(SEQ ID NO: 206)

MRGKVIYGTTLIGLFLFFYFWIPKHHIERIHHRIKVDAKSDLTGFKTHLPIS  
SIDTKQQVIVPLVTKEGGKYVKARDNINVDIELRDSPSRSHHLSEKPRIRTKGLIS  
YRGNSSRYFDKKSLKVKFVTNKLKEKKHRLAGMPKESEWVLHGPFLDRTLLR  
NYLSYNIAGEIMPMPQTFAVSYLSMVSIRE

25

Sequence description:

A] Length: 582 bp - 194 aa (Partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-113 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-113 gene sequence. ATG start codon is preceded by a Shine-Dalgarno sequence-Possesses a potential leader peptide sequence. C-terminus to be determined.

30

35

ID-181

5 Clone 2-17b (ID-117b)

(SEQ ID NO: 207)

CTTCACATTTATTGATCACTATCTGACAAATGTTAATCAAACAGCAGTTCT  
TATTTAGTGGATATTATTCAATGTATGTCTTGCAGACCTTAATTCAATAT  
10 TTTGGGAATCTCTTTGCGCGTGTCTTAGTATTGTTAGAGATATTCT  
GTAGAGATGCTTGCTAATATGGAAAGGCTAGGCATGTCTTATTGATA  
GGACACCGGCAGGATCTATTGTGTCACGTATTACTAATGATACTGAAGCAA  
TATCTGATATGTTTCGGGTATTTATCAAGTTTATCTCGGCGATATTAT  
15 TTTACAGTTACTCTGTACACTATGTTGATGCTAGACATTAAACTAACAGG  
ACTCGTCGCTCTTTGTTACCTGTTATCTTATATTAGTGAATGTCTATCGG  
AAAAAAATCAGTCACTGTCATTGCTAAAACGAGAAGTTACTTAGTGAATTC  
AACAGTAAATTATCAGAAAGTATTGAAGGAATTCT

(SEQ ID NO: 208)

20 SHFIDHYLTNVNQTAVLILVGYYSMYVLQLIQYFGNLFFARVSYSIVRDIRD  
AFANMERLGMSYFDRTPAGSIVSRITNDTEAISDMFSGILSSFISAIFIFTVTLYT  
MLMLDIKLTGLVALLPVIFILVNVYRKKSVTVIKTRSLLSDINSKLSEIESIEGI

25 Sequence description:

A] Length: 498 bp - 165 aa (Partial gene sequence)

30 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-117 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-117 gene sequence.  
N- and C-termini have yet to be determined

ID-182

35 Clone 3-8b (ID-120b)

(SEQ ID NO: 209)

40 ATGTACCATATTGAATTAAAAAAAGGAAGCTTACTACCAAGAGAACGGCT-  
AGTTGATTTAGGCGCAGATAGATTGAGTAATCAGGAGTTATTAGCCATTCT  
CTTACGTACAGGTATTAAAGAAAAACCTGTTCTGAAATTCAACGCAAAT  
TTTAGAAAACATAAGCAGTTAGCAGATTGGTCAATTATCCTTACAGGA  
GTTGCAATCCATTAAAGGAATCGGTCAAGGTTAAATCCGTCGAAATAAAAG  
CTATGCTAGAACTAGCAAAACGGATTCACAAAGCTGAATATGATCGTAAA

GAGCAAATTAAAGTAGTGAACAATTAGCGAGGAAAATGATGCTCGAATT  
AGGGGATAAAAAACAAGAACATTAGCTATTATGGATACACAAA  
ATCGTATTATCGAACAGAGAACTATTTATTGGTACTGTACGTCGTTCA  
5 TAGCAGAGCCAAGAGAAATTCTACATTATGCTTGTAAAAACATGGCAACT  
TCTTGATTATTATACATAATCATCCCTCAGGTTCTCCAAATCCCAGTGAAA  
GTGATTAAAGTTCACTAAAAAAATAAAACGATCATGTGATCATCTGGAA  
TTGTCTGCCTAGATCACATCATCGTTGGAAAAATAAATATTATAGTTTC  
GAGAAGAAGCAGATATTAA

10 (SEQ ID NO: 210)  
MYHIELKKEALLPRERLVDLGADRLSNQELLAILLRTGIKEKPVLEISTQILENI  
SSLADFGQLSLQELQSIKGIGQVKSVIEIKAMLEAKRIHKAEYDRKEQILSSEQ  
LARKMMLELGDKKQEHLVAIYMDTQNRIIEQRTIFIGTVRRSVAEPREILHYAC  
15 KNMATSЛИHNHPSGSPNPSESDSLFTKKIKRSCDHLGIVCLDHIVGKNKYYSF  
REEADIL\*

Sequence description:

20 A] Length: 681 bp - 227 aa (full-length gene)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-120 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-120 gene sequence.  
ATG start codon is preceded by an typical  
25 Shine-Dalgarno sequence. No obvious leader  
peptide sequence

ID-183

30 Clone 3-11b (ID-121b)

(SEQ ID NO: 211)

TGGTTAAAAGTAGTGATAGCTTGTATTCCATCTATTAAATTGCTTACCAT  
35 TTGATAATTGGTTGAAGCTCATTAAATTTCATGATTCCGATTGCAATAGC  
CCTAATCTTTATGGTTGTCTCATATGGGTTGAAAAACGTAATGCACAC  
CTCAAACCACAGTAACCGAATTGGCAAGTATGTCTTACAAGACAGCTTC  
TTGATTGGATGTTCCAGGTTCTCAGTATTGTTCCGGGAACCAGTCGTTCTG  
GAGCTACTATTAGGAGCAATTATTGGAACTAGTCGTTGGTCTG  
40 CTGACTTTACTTCTTCCATCCAACTATGTTGGTTATAGTGGACT  
TAAGGCGGTAAATATTAGATGGTAACGTCTGAGTTAGACCAATC  
TTAATACTTTAGTAGCAAGTCTGACAGCTTCGTAGTTAGTTATATGTT  
ATTCTGTTCTGACAGACTATGTCAAACGACACGATTCAACATCTTGGT

AAGTATCGTATAGTCTTAGGAAGTTACTCATCCTCTACTGGTTAGTTGTTC  
ATTTATTCTAA

(SEQ ID NO: 212)

5 WLKVVIACIPSILIALPFDNWFEAHFNFMPIAIALIFYGFVFIWVEKRNAHLKP  
QVTELASMSYKTAFLIGCFQVLSIVPGTSRSGATILGAIIGTSRSVAADFTFFLA  
IPTMFGYSGLKAVKYFLDGNVLSLDQSLILLVASLTAFVVSLYVIRFLTDYVKR  
HDFTIFGKYRIVLGSLLILYWLVVHLF\*

10

Sequence description:

A] Length: 579 bp - 193 aa (partial sequence)

15 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-68 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-68 gene sequence  
described in WO 00/06736. N-terminus has yet to be determined.

20 ID-184

Clone 3-11c (ID-121c)

(SEQ ID NO: 213)

25 ATGGAAATGAAACAAATCACTGAAACAAACACTGAAAATTACAATTAGTAT  
GGAAGATTAGAAGATCGTGGTATGGAGCTGAAAGATTCCCTAATCCCTCA  
GGAGAACAGACTGAGGAATTTCTATTCTGTATGGATGAATTAGACTTGCC  
AGAAAACTTAAAAATAGTGGTATGTTAAGTTTCGAGTAACACCTAAAA  
AAGATCGCATTGATGTTTGTACAAAGTCTGAATTAAAGTAAAGATTAA  
30 ATTTAGAAGAATTAGCAGATTGGGTGACATTCAAAATGTCTCCAGAAG  
ACTTTTTAAAACCTTGGAACAAATCGATGTTGGAAAAAGGGGATACGGAT  
GCCCATGCCAAATTAGCAGAAATTGAAAATATGATGGATAAAGCAACTCA  
AGAAGTAGTTGAGGAAAATGTTCTGAAGAACACCTGAAAAGGAAGTAG  
AAACGATTGGATATGTTCACTATGTCTTGATTGATAATATTGAAGCTGT  
35 AGTCGATTTCACAAACGATTGATTTCACAAATAGAAGCTT

(SEQ ID NO: 214)

40 MEMKQISETTLKITISMEDLEDRGMELKDFLIPQEKEEFFYSVMDELDLPENF  
KNSGMLSFRVTPKKDRIDVFVTKSELSKDLNLEELADLGDISKMSPEDFFKTLE  
QSMLEKGDTDAHAKLAEIENMMKDATQEVEENVSEEQPEKEVETIGYVHY  
VFDFDNIEAVVRFSQTIDFPIEA

Sequence description:

A] Length: 547 bp - 182 aa (Partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
5 identified downstream of the ID-68 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-68 gene sequence.  
ATG start codon is preceded by an typical  
Shine-Dalgarno sequence. No obvious potential  
leader peptide  
sequence

10

ID-185

Clone 3-16b (ID-122b)

15

(SEQ ID NO: 215)

20

GGAAACCAACGCCAGTACAATCGTCAAGGGTAGATTATCCTAACGTAG  
TCGTGCCAAGATTGAGAAGTTATTTAGACAAGCTTCTACTACTGATTA  
TTCTGGTGTACAAAGGTTACTATATTGACTTGAAGCCAAAGAAACCCG  
GCAGAAAAGTCTATGCCTATGAAAAATTTCATGCTCACCAAATAGAGC  
ACATGGCAAATGTATTACAGCAAAAGGGATTGCTTGCTTGTCTGCTTCATT  
TTTCCACACTTAAGGAAACCTATCTACTCCCTGCTAATGAGTTAATTTCATT  
TTATCAGATTGATAAAGGCAATAATCAATGCCTATTGATTATATCAGAAA  
AAATGGATTTCGTAAAGGAGAGTGCCTTCCTCAAGTCCCTACTTAGA  
25 TATTATTGAAGAAAAATTATTAGGCGGTGATTACAATTAA

25

(SEQ ID NO: 216)

30

GNQRPVQSSRVDYPKRSRAKIVEVYFRQASTTDYSGVYKGYYIDFEAKETRQ  
KTAMPMKNFHAHQIEHMANVLQQKGICFVLLHFSTLKETYLLPANELISFYQI  
DKGNKSMPIDYIRKNGFFVKEAFPQVPYLDIIEKLLGGDYN\*

Sequence description:

35

A] Length: 447 bp - 149 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was  
identified upstream of the ID-122 gene which was identified by LEEP, during  
cloning and sequence analysis of the full-length ID-122 gene sequence. N-  
terminus has yet to be determined

40

ID-186

Clone 3-17b (ID-123b)

(SEQ ID NO: 217)

5           GGATCCTAAAAACGCTAAGGTTATCAAAAAAAATGCTGATCAATTAGTG  
ACAAGGCAATGGCTATTGCAGAGAAGTATAAGCCAAAATTAAAGCTGCA  
AAGTCTAAATACTTGTGACTTCACATACAGCATTCTCATACTTAGCTAAG  
CGATACGGATTGACTCAGTTAGGTATTGCAGGTGTCTCAACCGAGCAAGA  
ACCTAGTGCTAAAAAAATTAGCCGAAATTAGGAGTTGTGAAAACATATA  
AGGTTAAGACTATTTTGTGAAGAAGGAGTCTCACCTAAATTAGCTCAAG  
10          CAGTAGCTTCAGCTACTCGAGTTAAATTGCAAGTTAACAGCTTAAAG  
CAGTTCCCAAAAACAATAAAGATTACTTAGAAAATTGGAAACTAATCTTA  
AGGTACTTGTCAAATCGTTAAATCAATAG

(SEQ ID NO: 218)

15          DPKNAKVYQKNADQFSDKAMAIKEKYKPKFKAASKYFVTSHTAFSYLAKR  
YGLTQLGIAGVSTEQEPESAKKLAEIQEFVKTYKVKTIFVEEGVSPKLAQAVAS  
ATRVKIASLSPLEAVPKNNKDYLENLETNLKVLVKSLNQ\*

20          Sequence description:

20          A] Length: 433 bp - 144 aa (partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-123 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-123 gene sequence.  
25          N-terminus has yet to be determined

ID-187

30          Clone 3-46/47 (ID-130b)

(SEQ ID NO: 219)

35          ATGAAAAAAAGTCATCGATTAAAAAAACTACAAAAAGCATACGCCTCAGA  
AACTGTTTAAATAATATTAAATTGGAGGTGTTAAAGGAGAAATAATTGG  
ATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTGATTAAAATATGCT  
TGGCATGGAAAAAGCAGATAAGGGAACAGCTCTGTTCTGATACTCAAA  
TGCCAGATCGTAATATTTAAATCAAATTGGCTATATGGCTCAATCTGATG  
CCTTACACGAGTCTTAACCTGGCTAGAAAATTATTATTCTTGGAAAAAA  
40          TGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACTCATATTCT  
AAAGTAGTAGATCTAGAAAACCAACTTGATAAATTGTCTCAGGTTACTCA  
GAAGGTATGAAAAGACGGCTTCTAGCCATGCCCTACTTGGAAACCCCC  
ACAGTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTGAGG  
AGAAAAAATCTGGCAAGAGCTAATTAATTAAGGATGAAGGACGTTCTAT  
CTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGC

ACTACTATTACGTGGAAACATTATTGCCTTGATACTCCATTACATTAAA  
AAAACAATTAAATGTGAGTACTATTGAGGAAGTTCTAAAAGCTGAAGG  
AGAATAA

5 (SEQ ID NO: 220)  
MKKVIDLKKLQKAYASETVNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGME  
KADKGTLVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLFFGKMKGIQ  
KTELKQQITHISKVVVDLENQLDKFVSGYSEGMKRRSLAIALLGNPTVLILDEP  
10 TVGIDPSLRRKIWQELINIKDEGRSIFITTHVMDEAELETSKVALLRGNIIAFDTP  
LHLKKQFNVSTIEEVFLKAEGE\*

Sequence description:

15 A] Length: 717 bp - 239 aa (Possible full-length sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified upstream of the ID-130 gene which was identified by LEEP, during  
cloning and sequence analysis of the full-length ID-130 gene sequence. ATG  
start codon is preceded by a possible  
20 Shine-Dalgarno. No obvious potential leader  
peptide sequence

ID-188

25 Clone 3-83b (ID-144b)

(SEQ ID NO: 221)

30 ATGGTACAAATGATACTGATATGATTAAAACAATTGAGCATTGCTGAG  
ACACAAGCTGATTTCCAGTGTATGATATTTAGGGGAAGTCACACTTAT  
GGACAACCTAAAGTAGACTCTGACTCTAGCTGCTCATATTGATAGCCTA  
GGCCTTGTGAAAAATCACCTGTCTTAGTATTGGTGGTCAAGAATATGAA  
ATGTTGGCGACATTGTTGCTTAACAAAGTCAGGGCATGCTTATATACCG  
35 GTTGACCAACACTCTGCTTGGATAGAACATACAGGCTATTATGACAGTTGCT  
CAACCAAGCCTTATCATTCAATTGGTAATTCCCTCTGAAGTTGATAAT  
GTCCCCAATCCTAGACGTTCTCAAGTTCAGCTATTGAAAGAAAAGACT  
CCTTATGAGGTAACACATTCTGTTAAAGGTGATGATAATTACTATATTATT  
40 TTCACCTCAGGGACTACTGGTTACCAAAAGGTGTGCAAATTACATGAC  
AATTATTGAGCTTACAAATTGGATGATTCTGATGATGAGTTTCAGTTC  
CTGAAAGACCGCAAATGTTGGCTCAACCC

(SEQ ID NO: 222)

MVQMIHDMIKTIEHFAETQADFPVYDILGEVHTYQLKVDSDSLAAHDSLGL  
VEKSPVLVF GGQEYEMLATFVALTKSGHAYIPVDQHSALDRIQAIMTVAQPSL

IISIGEFPLEVNVPILDVSQVSAIFEKTPYEVTHSVKGDDNYYIIFTSGTTGLP  
KGVQISHDNLLSFTNWMISDDEFSVPERPQMLAQP

5 Sequence description:

- A] Length: 592 bp - 197 aa (partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
10 identified downstream of the ID-144 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-144 gene sequence.  
Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. No obvious  
15 leader peptide sequence  
This orf is not in frame with nuc

ID-189

20 Clone 3-86b (ID-145b)

(SEQ ID NO: 223)

ATGGAAAATCATCGTTATGAAGATGAAGGTAAATTCCAGCGTAAGATGAC  
CAGTCGTACATCTCTTATGTTATCGCTAGGTGGTGTATCGGGACTGGGCTT  
25 TTCTTGAGTTCAAGGTATACCATTGCACAGGCTGGTCCGCTGGAGCTGTG  
CTGTCTTATTGATTGGTGCCGTGTTATTGGTCATGCTATCACTTG  
GGGAATTGGCGGGTGCATGCCGGTGACGGGGTCAATTCCACACTTATGCCA  
CTAAGTTATCAGTCCTGGAACAGGTTTACTGTTGCTTGGCTATATTGGAT  
30 TTGTTGGACGGTCGCCTGGGGACTGAATTAGGTGCTGCCATGCTGAT  
GCAGCGCTGGTCCCCTGGGACTGAAATTAGGTGCTTGGCTATGGAT  
CTTGTGATTGGTTAAATGCTCTAGCGTACGCTTTGCAGAACAGCAG  
AGTCTTCTCAAGTATTAAGGTATTGCTATCATTATCTTATTATCTTG  
GGCTTAGGTGCTATGTTGGTCTAGTTCCCTTGAAGGTCAAGCACAAAGGCT  
ATTCTCTCACTCATGACTGCCAATGGTGCCTTCCAAATGGTATCGTTG  
35 CAGTTGTCTCAGTCATGTTGGCTTTAACTATGCCCTCTGGTACTGAGTT  
AATTGGTATTGCGGCTGGTGAAACGGATAATCCCAAAGAACAGCTGTACCAA  
GGGCTATTAAAACGACAATCGGTCGCTGGTTGTTCTTGTACTGACAA  
TTGTTGTCCTAGCTTCGCTATTGCCAATGAAAGAGGCAGGCATCCACAG  
CACCAATTGCGTGTGACAAAGATGGGAATCCCTTACGGCGGATA  
40 TCATGAACCTCGTTATCTTGACAGCCATCCTGTCTGCTGGTAACTCAGGTCT  
CTACGCATCAAGCCGTATGCTCTGGTCCCTGCCAATGAAGGTATGTTGTC  
AAAATCTGTTGTGAAAATCAATAAACACGGTGTCCAATGCGTGCTCTTCT  
CTTGTCAATGGCAGGAGCAGTGCTGTCGCTTTCAAGTATTACGCTGC

AGACACAGTTATCTAGCCTGGTTCAATCGCGGGCTTGCTGTTGTC  
GTATGGCTAGCCATTCCAGTCGCACAAATCAATTCCGCAAGGAATT

(SEQ ID NO: 224)

5 MENHRYEDEGKFQRKMTSRHLFMLSLGGVIGTGLFLSSGYTIAQAGPLGAVL  
SYLIGAVVVYLVMLSLGELAVAMPVTGSFHTYATKFISP GTGFTVAWLYWIC  
WTVALGTEFLGAAMLMQRWF PNVP AWAFASFFALVIFGLNALSVRFFAEAES  
10 FFSSIKVIAIIIIFIILGLGAMFGLVSFEGQHKAILFTHLTANGAFPNGIVAVVSVM  
LAVNYAFSGTELIGIAAGETDNPKEAVPRAIKTTIGRLVVFFVLTIVVLASLLPM  
KEAGVSTAPFVDVFDKMGIPFTADIMNFVILTAILSAGNSGLYASSRMLWSLA  
NEGMLSKS VVKINKHGVPMRALLSMAGA VLSLFSSIYAADTVYLA LVIAGF  
AVVVVWLAIPVAQINFRKEF

15 Sequence description:

A] Length: 1126 bp - 393 aa (partial gene sequence)

20 B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-145 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-145 gene sequence. Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possesses a  
25 possible leader peptide sequence.

ID-190

30 Clone 3-94b

(SEQ ID NO: 225)

TCAGAAAATGCAGAGGCAGCAACGGTTGCCACAAACTGGTTACCAAAGG  
AGCTAATGTCATTATCGGACCAGCAACATCGGGTGCAGCTGCATCTTCAAC  
35 TCCAAAAGTAAATGCAGCAGCAGTTCCAATGATTGCACCTGCTGCGACAC  
AAGACAATTAGTCTATGGTTCTGATGGAAAAAACCTTAAATCAGTATTCT  
TCCGAGCTACTTTGTCGATAATTATCAAGGAAAGCTATTGTCTCAGTATG  
CTACAGACAACCTTAAAGCTAAAAAGTTGTTCTATTTATGATAATTCA  
40 CAGATTACTCAAAGGGGGTAGCAAAATCATTAAAGGAAAGTTATAGTGGAA  
AAAATTGTTGATAGTATGACATTCTCCGCTGGTGATACTGATTCCAAGCG  
TCATTGACTAAGTTGAAAGGGAAAGAATATGATGCTATTGTGATGCCAGG  
TTACTATACCGAGACAGGATTAATAGTTAAGCAAGCGCGT GATTTAGGTAT  
CTCTAAACCGGTTCTGGGCCTGATGGTTTGATAGTCCGAAATTGTGCA

ATCGGCAACACCTGTAGGAGCTCAAACGTTATTATTGACAGGTTCAC  
TACACAAGGATCAACCAAAGCTAAAGCT

(SEQ ID NO: 226)

5 SENAEAATVATNLVTKGANVIIGPATSGAAASSTPKVNAAA VPMIAPAATQD  
NLVYGS DGKTLNQYFFRATFVDNYQGKLLSQYATDNLAKKVVLFYDNSSD  
YSKGVAKSFKESYSGKIVDSMTFSAGDTDFQASLTKLKGKEYDAIVMPGYYT  
ETGLIVKQARDLGISKPV LGPDGF DSPKFVQSATPV GASNVYYLTGFTTQGST  
KAKA

10

Sequence description

15 A] Length: 637 bp - 231 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-149 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-149 gene sequence. N- and C-termini have yet to be determined

20

ID-191

Clone 2-c94b (ID-153b)

25

(SEQ ID NO: 227)

TTGGGACTTAAAGACCATGCTTAGTCTATCCATTTCATTATCTGGGGGG  
CAAAAGCAACGTGTCGCACTAGCTCGTGCATGATGATTGATCCACAGATT  
ATTGGTTATGATGAGCCA ACTAGCGCTCTTGATCCAGAGTTGCGTCAAGAA  
30 GTAGAAAAACTAATTTACAAAATAGAGAACAGGTATGACACAAATTGT  
AGTAACACATGATCTCAATTGCTGAAAGTATCTGATA CGATTCTCAA  
AATTAATCCTAAGTAG

(SEQ ID NO: 228)

35 MGLKDHALVYPFSLSGGQKQRVALARAMMIDPQIIGYDEPTSALDPELRQEV  
EKLILQNRETGMTQIVVTHDLQFAESISDTILKINPK\*

40 Sequence description

A] Length: 270 bp - 90 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-153 gene which was identified by LEEP, during cloning and sequence analysis of the ID-153 gene sequence.

N-terminus has yet to be determined

5

ID-192

Clone 2-c1b (ID-155b)

10

(SEQ ID NO: 229)

ATGACTAATATCTCAGATGTTCCAAAAGCTATTAGAACACAGGCACAGTAT  
GTTCTCTGGGAATGAGAGTTATGGATCAGTCGGTATTACCGAAAACATAT  
AATTCAAAAGAACCTTATTGAAACCAGATATGATTATATTGATAGA  
15 AGACAAGAGACAATGCTTAAAATCACTCAAGAAATAGAAATGGAGCATTG  
A

(SEQ ID NO: 230)

MTNISDVPKAIRTQAQYVLLGMRVMDQSVLPKTYNSKEPYLKPDIMIYIHDRR  
20 QETMLKITQEIEMEH\*

Sequence description

25

A] Length: 204 bp - 68 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-155 gene which was identified by LEEP, during cloning and sequence analysis of the ID-155 gene sequence.

30

ATG start codon is preceded by a potential typical Shine-Dalgarno sequence.

Has a

typical leader peptide. N-terminus has yet to be verified

35

ID-193

Clone 2-54altb (ID-172b)

40

(SEQ ID NO: 231)

AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCTTGGGGAAATATAAATT  
TGGATTCATGACGATGTAAAGCCAATTATTCTACGGGAAAAGGTCTAAA  
TGAGGCTGTTATCGTGAGTTATCTGCAGCTAACGGTGAACCTGAGTGGAT  
GTTGGACTTCTGCTAAAATCCTGGAAACGTTAATAAAATGCCGATGCA

GACCTGGGGAGCAGATTATCAGATATTGATTTGATGATATTATTATTA  
TCAAAAAAGCATCTGATAAACCTGCGCGTGATTGGGATGATGTTCCAGAAA  
AAATCAAAGAAACTTTGAAAGAATTGGGATTCCAGAAGCTGAAAGAGCC  
TATCTGCAGGAGCATCAGCACAAATATGAATCAGAAGTAGTTATCACAAT  
5 ATGAAAGAAGAATATGATAAGCTGGGTATTGTTTACGGATACTGACTCT  
GCACTTAAAGAGTACCCAGAGCTATTCAAAAAATATTTGCTAAACTTGTC  
CCTCCAACAGATAATAAATTAGCTGCTCTGAACCTGCTGTATGGTCAGGT  
GGAACATTATTATGTTCTAAAGGTGTTAAGGTGGATATTCCACTTCAA  
ACTTACTTCCGTATTAATAATGAAAATACTGGACAATTGAACGTACTCTC  
10 ATTATTGTTGATGAGGGAGCAAGTGTCACTATGTTGAAGGTTGTACCGCC  
CCAACCTATTCTCAAATAGTTACATGCAGCTATAGTTGAAATTTCGCAC  
TTGATGGAGCTTATATGCGCTATACGACTATTCAAAATTGGTCCGATAATG  
TCTATAATTAGTGACAAAACGTGCTACCGCTAAAAAGATGCAACAGTT  
15 GAGTGGATAGATGGAAATCTAGGAGCTAAAACAACAATGAAATACCCATC  
GGTTTACCTTGATGGTGAAGGAGCACGTGGCACGATGTTGTCTATTGCTTT  
TGCAAACAAAGGACAACACCAAGATACTGGGTGCAAAGATGATTATAATG  
CCCCCCCATACTAGTTCATCCATTGTCTAAATCAATTGCTAAGGGTGGGG  
GAAAAGTTGATTATCGAGGTCAAGTGACATTAAATAAGATTCCAAAAAA  
TCAGTGTACATATAGAATGTGACACCATTGATGGATGATATTCAA  
20 TCAGATACCATAACCGTTAATGAGATTATAATTCACAGGTTGCTTAGAG  
CATGAAGCAAAGGTGCTAAGATTCTGAAGAGCAACTGTACTACTGATG  
AGTCGAGGTTATCTGAAGCTGAAGCAACAGAAATGATTGTTATGGGTT  
GTTGAGCCCTTACGAAAGAATTACCAATGGAATATGCGGTAGAGTTAAA  
TCGTTAATTCTATGAAATGGAAGGTTCAGTTGGTTAA  
25  
(SEQ ID NO: 232)  
MHACRSTLEDLGEYKFGFHDDVKPIYSTGKGLNEAVIRELSAAKGEPEWMLD  
FRLKSLETFNKPMPMQTWGADLSDIDFDDIYYQKASDKPARDWDDVPEKIKE  
TFERIGIPEAERA YLAGASAQYESEVVYHNMKEEYDKLGIVFTDTDSALKEYP  
30 ELFKKYFAKLVPPTDNKLAALNSAVWSGGTFIYVPKGVKVDIPLQTYFRINNE  
NTGQFERTLIIVDEGASVHYVEGCTAPTYSSNSLHAAIVEIFALDGAYMRYTTI  
QNWSNDNVYNLVTKRATAKKDATVEWIDGNLGAKTTMKYPSVYLDGEGARG  
TMLSIAFANKGQHQDTGAKMIHNAPHTSSSIVSKSIAKGGGKVDYRGQVTFN  
KDSKKSVSHIECDTILMDDISKSDTIPFNEIHNSQVALEHEAKVSKISEEQLYYL  
35 MSRGLSEAEATEMIVMGFVEPFTKELPMEYAVELNRLISYEMEGSVG\*

Sequence description:

- 40 A] Length: 1411 bp - 469 aa (Possible full-length gene)  
B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-72 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-72 gene sequence. No obvious Shine Dalgarno sequence upstream of

TTG start codon insufficient sequence data). N terminus needs verification.

5 ID-194

Clone 3-1b (ID-81b)

(SEQ ID NO: 233)

10 ATGATAGAATTCTTCTAATATCAGAACAGAGATTCCGCAGATGCCTTA  
CTTATCCATAGTTGATTATCTGTCTACCTTCTGATGTGGCTGACTTT  
GGTTAATAGAGATAAGCCTTGTATAAAACTATTGGAGTATCCTTTAGG  
ACTTCAGTTAATTACGATTATACTGGTTTCTGGGAAAATTGCCTTA  
15 TCTGAAAGTCTCCCCTTACCATGTCGAATAGGCATGTTGTCGGTCTCT  
TA

(SEQ ID NO: 234)

MIEFFSNIRTEIPQMPLLHSILSVPFLMWLTVNRDKPLYKTIWSILLGLQLI  
TIYTWFYWAKLPLSESLPLYHCRIGMFVGLL

20

Sequence description

A) Length: 261 bp - 87 aa (partial gene sequence)

25 B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-81 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-81 gene sequence. Sequence Characteristics: Possesses a potential leader peptide sequenceOrf is preceded by a potential Shine-Dalgarno sequence.

30

ID-195

Clone RS-55b

35

(SEQ ID NO: 235)

AAGCTTGTGCAAAGTATTAAAGAGATAGGATTAGCTAATGCGCATTATT  
GCTGTTGCTCCGACAGGGTCAATCAGTTATCTTCTTGTACTCCGAGCC  
TTCAACCGGTTGTATCACCTGTCGAAGTACGCAAGGAAGGAGCACTGGGG  
AGGGTTATGTAGCTGCTTATAAGATTGATGCAGATAATTATGTCTACTAC  
40 AAAAAAAGGAGCTTATGAAGTGGGATCTGAGGCGATTATCAATATTGCAGC  
TGCCGCTAAAAACACATTGATCAAGCTATTGTTAACGCTTTCATGAC  
AGATCAAGCAACTACGCGAGATTAAATAAGCCTATATTCAAGCATTAA  
AACAAAAATGTGCCTCTATTATTATGTACGAGTGAGACAGGACATCCTAG

AAGGTAGCGAGAGTTATGATATGCTGGATGATTCACTTCATCGGACT  
TAGAAGACTGTCAATCCTGCATGATTAA

(SEQ ID NO: 236)

5 KLVQSIKEIGLANAHLLAVAPTGSISYLSSCTPSLQPVVSPVEVRKEALGRVY  
VAAKYKIDADNYVYYKKGAYEVGSEAIINIAAAAQKHIDQAISLTLFMTDQATT  
RDLNKAYIQAFKQKCASIYYVRVRQDILEGSESYDDMLDDFTSSDLEDCQSC  
MI\*

10

Sequence description:

A] Length 486 bp - 162 aa (Partial sequence)

15 B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-87 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-87 gene sequence. N-terminus to be determined.

20 ID-196

Clone RS-59(ID-90b)

(SEQ ID NO: 237)

25 GTGAGGACATATATTACAAACTTGAATGGACATTCAATCACTAGTACAGC  
ACAAATAGCTAAAACATGGTAACAGATATAGCAGTAAGCTTAGGTTTC  
GTGAGCTGGAAATACATTCTATCCGATTGATACTGATTCTCCTGAGGAAA  
TGAGTAAGCGTTAGATGGAATCTGTTCCGGACTTAGAAAAAAATGATATTG  
TCATATTCAGACACCTACATGGAACACTACAACATTGATGAAAAAATTAT  
30 TTCACAAATTAAAAATATTGGTGTAAAGATTGTTATTTTATACATGATGT  
TGTACCGCTAACATGTTGATGGAAATTTTATTTGATGGATAGAACTATAGC  
TTATTATAATGAAGCAGATGTTAATAGCCCCTAGTCAAGCAATGGTCGAT  
AAGCTT

35

(SEQ ID NO: 238)

MRTYITNLNGHSITSTAQIAQNMVTDIAVSLGFRELGIHSYPIDTDSPEEMSKRL  
DGICSGLRKNDIVIFQTPTWNTTFDEKLHKLKIFGVKIVIFIHDVVPLMFDGN  
FYLMMDRTIAYYNEADVLIAPSQAMVDKL

40

Sequence description:

A] Length: 414 bp - 138 aa(partial gene)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-90 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-90 gene sequence. No obvious signal peptide, but a  
5 possible Shine Dalgarno sequence is present upstream of ATG start codon. C-terminus has yet to be determined.

10 ID-197

Clone RS-59c (ID-90c)

(SEQ ID NO: 239)

CATGGAAATGAAGTTGATGATGTTATTAGAAGGGCATTGAATATAATCAC  
15 CTTATCTTGCTTTGATAATACCTGTACATAACAGAGAGTTAGTATTAGATA  
GCAATATCATTTCTCACACAACCTGTGAACAATTGATAAAATTAAATGAAAAA  
ATTATCAGGCTCCATTATGTATTGCTAGAGCAACAAAGAGAACAAACA  
20 AGTAATGAAACAAAAGAGCGTTATAAAGAAATTAGGAGGGTATGGAA  
ATGCCTAA

(SEQ ID NO: 240)

HGNEVDDVIRRAFEYNHLIFAFDNTCHNRELVLDNSIISHTCEQLINLMKNLS  
GSIMYLLEQQREQTSNETKERYKEILGGYGNA\*

25

Sequence description:

A] Length: 261 bp - 87 aa(partial gene sequence)

30 B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-90 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-90 gene sequence. N-terminus has yet to be determined

35

ID-198

Clone RS-70b (ID-93b)

(SEQ ID NO: 241)

ACATTTTATATTATGTATTGAAGACGTAGCCACCCAGTCAAATATGACT  
GGGAAGATTTAGTATGTCTAAAGAAGAGTTGTATATTACCCGTTATT  
AAACTTTAAGAATCAAGGTGTATACAACGGCTTGATTGGTCTATTCCTC  
CTTATGGGTTATATATTACAGAATCAAGAAATTGTAGCTATTTTTAA

TCAATGTGTTGCTAGTGCTGTTATGGTGCTTGACAGTTGATAAAAAAA  
TCTTATTAAAACAGGGTGGTTACCTATATTAGCTCTTTAACATTCTTATT  
TTAA

5 (SEQ ID NO: 242)  
TFLYYVFEDVATQSNMTGKIFSMSKEELSYLPVIKLFKNQGVYNGLIGLFLY  
GLYISQNQEIVAIFLINVLLVAVYGALTVDKKILLKQGGLPILALLTFLF\*

10 Sequence description:

A] Length: 312 bp - 104 aa (partial gene sequence)  
B] This gene sequence was not identified using the LEEP system. It  
was identified upstream of the ID-93 gene which was identified by  
15 LEEP, during cloning and sequence analysis of the full-length ID-93  
gene sequence.  
N-terminus has yet to be determined

20 ID-199

Clone RS-70c (ID-93c)

(SEQ ID NO: 243)  
25 ATGAAATTAAGTGCCTGATTATGGGCTTATTGATTATGGAAAAACTGCA  
AGTGATGCAATAACAAGAACGATTCTTTATCACAAAGAGGCAGCAACT  
AGGCTATCATCAATTGGGTGGCTGAACATCACGGTGTAAAGGCATTCAAG  
TATTAGCAATCCAGAATTAAATGATAATGCATTGGCTAACCAAGACTAAATC  
TATCAAAATTGGCTCTGGAGGTATAATGCCTCTGCACTATAGTAGTTAA  
30 ACTCGCGGAGACTCTCAAGACATTAGAGACATGTCATCCGAATCGAGTAA  
GTATTGGTTAGGAAATTCACTAGGGACAGTTAAAGTTCAAATGCACTTC  
GTAGCTTACATAAAGCACATGATTACGAAGAGGTACTGGAGGAATTGAAG  
TCATGGCTTATTGATGAATCATCCAGTAAGGAACCATTAGTTCAACCGACT  
35 CTTCTAGCTTCCCAGACTTATATGTGTTGGGAGTGGTCAAAAATCAGCT  
TATTAGCGGCTAAACTGGCTTAGGCTTACCTCGGTGTTTCCTTTA  
TGGACAAAGACCCATTGACAGAAGCTAAA

(SEQ ID NO: 244)  
40 MKLSVLDYGLIDYGKTASDAIQETILLSQEAEQLGYHQFWVAEHHGVKA  
NPELMIMHLANQTKSINKIGSGGIMPLHYSSFKLAETLKLETCHPNRVSIGLGN  
SLGTVKVSNALRSLHKAHDYEEVLEELKSWLIDESSSKEPLVQPTLSSFPDLYV  
LGSGQKSAYLAAKLGLGFTFGVFPMDKDPLTEAK

Sequence description:

5

A] Length: 588 bp - 196 aa (partial)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence. No obvious signal peptide, but Shine Dalgarno sequence upstream of the ATG start codon.



Figure 2

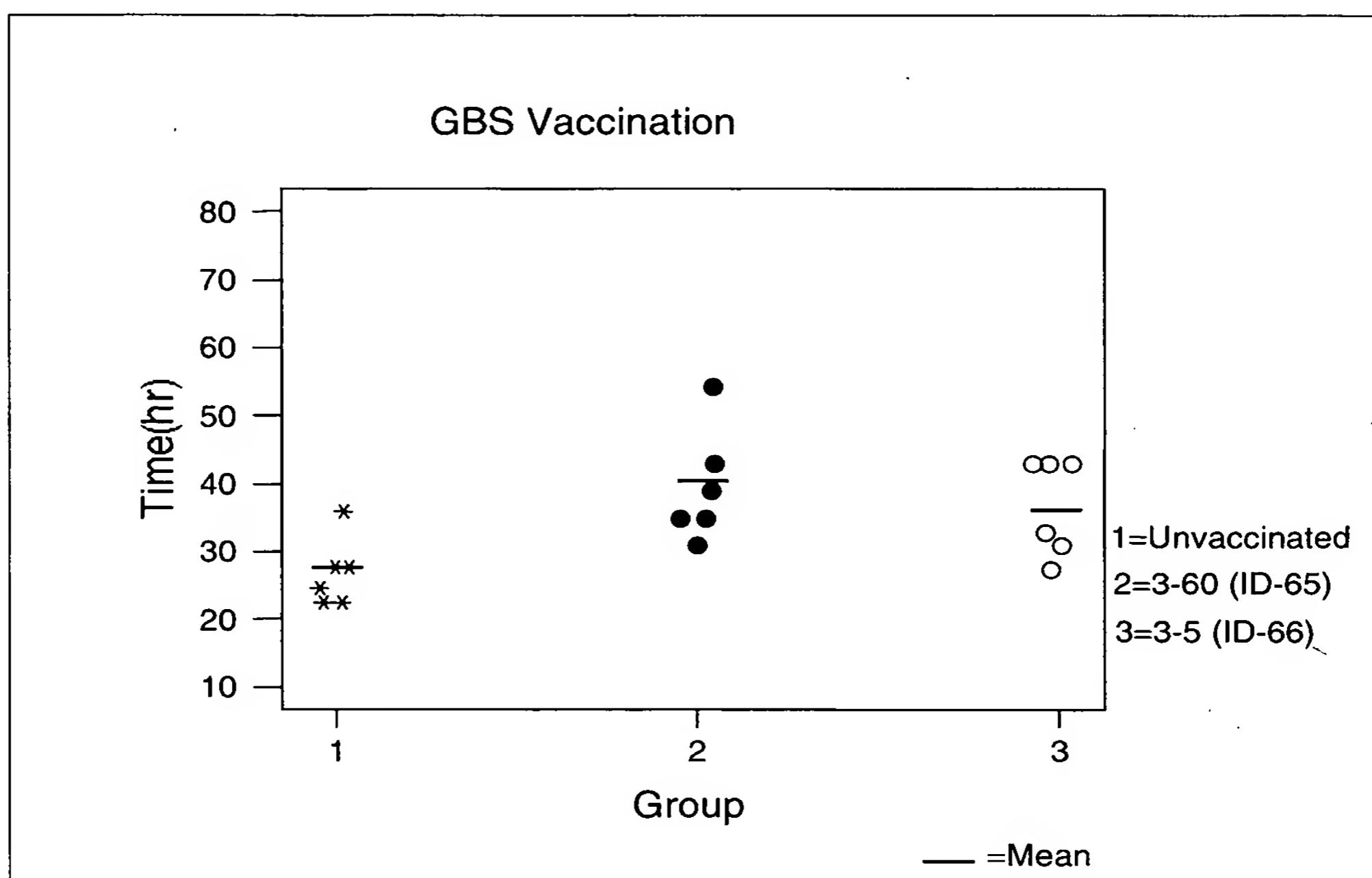




Figure 3

nucS1

Bgl II Eco RV

5'-cgaattctqatattccacaaacagataaacggcgtaatag -3' (SEQ ID NO.: 245)

nucS2

Bgl II Sma I

5'-gaattttccccggatcacaaacagataacggcgtaa-3' (SEQ ID NO.: 246)

nucS3

Bgl II Eco RV

5'-cgaattctqatattccatcacaaacagataacggcgtaa-3' (SEQ ID NO.: 247)

nucR

Bam HI

5'-cgatccttatggacctgaatcgttg -3' (SEQ ID NO.: 248)

NucSeq

5'-ggatgctttgtttcagggtgtac -3'

(SEQ ID NO.: 249)

pTREP<sub>F</sub>

5'-catgatatcggtacctcaagtcattatcattgtccggcaatggtgtggcctttttttttttagcgatacaatttcacac -3' (SEQ ID NO.: 250)

pTREP<sub>R</sub>

5'-gcggatccccgggtttttaatatgtttaaacactagtcgaagatctcgcaatttctctgtgtaaattt  
gtttatccgtta -3' (SEQ ID NO.: 251)

pUC<sub>F</sub>

5'-cgcagggttttcccagtcacac -3'

(SEQ ID NO.: 252)

V<sub>R</sub>

5'-tcagggggggcggagcctatg -3'

(SEQ ID NO.: 253)

V<sub>1</sub>

5'-tcgtatgttgtgtggaatttg -3'

(SEQ ID NO.: 254)

V<sub>2</sub>

5'-tccggtcgatgttgtgtggaatttg -3'

(SEQ ID NO.: 255)



**Figure 4**

**pTREP-Nuc vectors allow cloning of genomic DNA into each frame with respect to the nuclease gene**

5

{1}

Cloning site is indicated by an arrow

(SEQ ID NO.: 259)

The diagram illustrates the map of the pTREP1-nuc vector. It features two concentric circles. The inner circle contains the following labels: 'rep' at the bottom left, 'pTREP1-nuc' in the center, 'MLS' at the bottom right, and 'Tn4430' at the bottom. The outer circle contains labels for restriction sites: 'KpnI EcoRI' at the top left, 'EcoRV or SmaI' at the top center, 'BamHI 668' at the top right, 'XbaI PstI' on the right side, and 'BgIII' at the very top. A large black arrow points from the label 'Expression cassette' to the 'nuc' gene, which is located between the KpnI/EcoRI site and the BamHI site.

The diagram illustrates the pTREP-nuc Cassette. It features a long horizontal bar representing the nucleic acid sequence. On the left, a transcription terminator is indicated by a black box with a diagonal line. Below it, a sequencing primer is shown as a vertical arrow pointing towards the cassette. The cassette itself consists of several segments: a P1 promoter (indicated by a small black box), followed by a white box labeled "nuc", and another black box representing a transcription terminator. Above the cassette, four restriction enzyme sites are marked with vertical lines: Kpn I on the far left, Eco RI, Bgl II, Sma I or Eco RV in the middle, and Pst I on the far right.



**Figure 5**

**SDS-PAGE analysis of the purified ID-65 and ID-83 protein antigens**

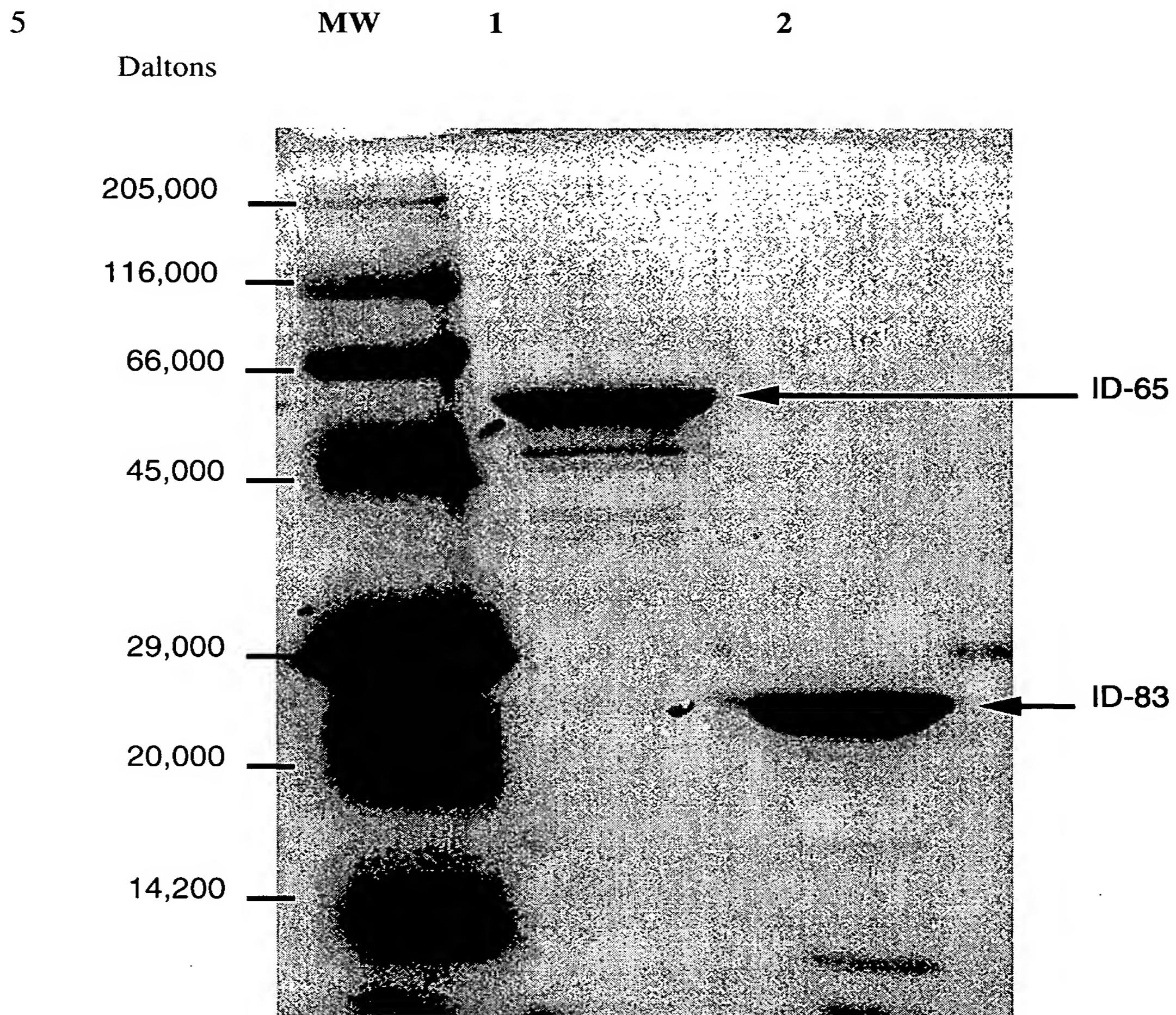
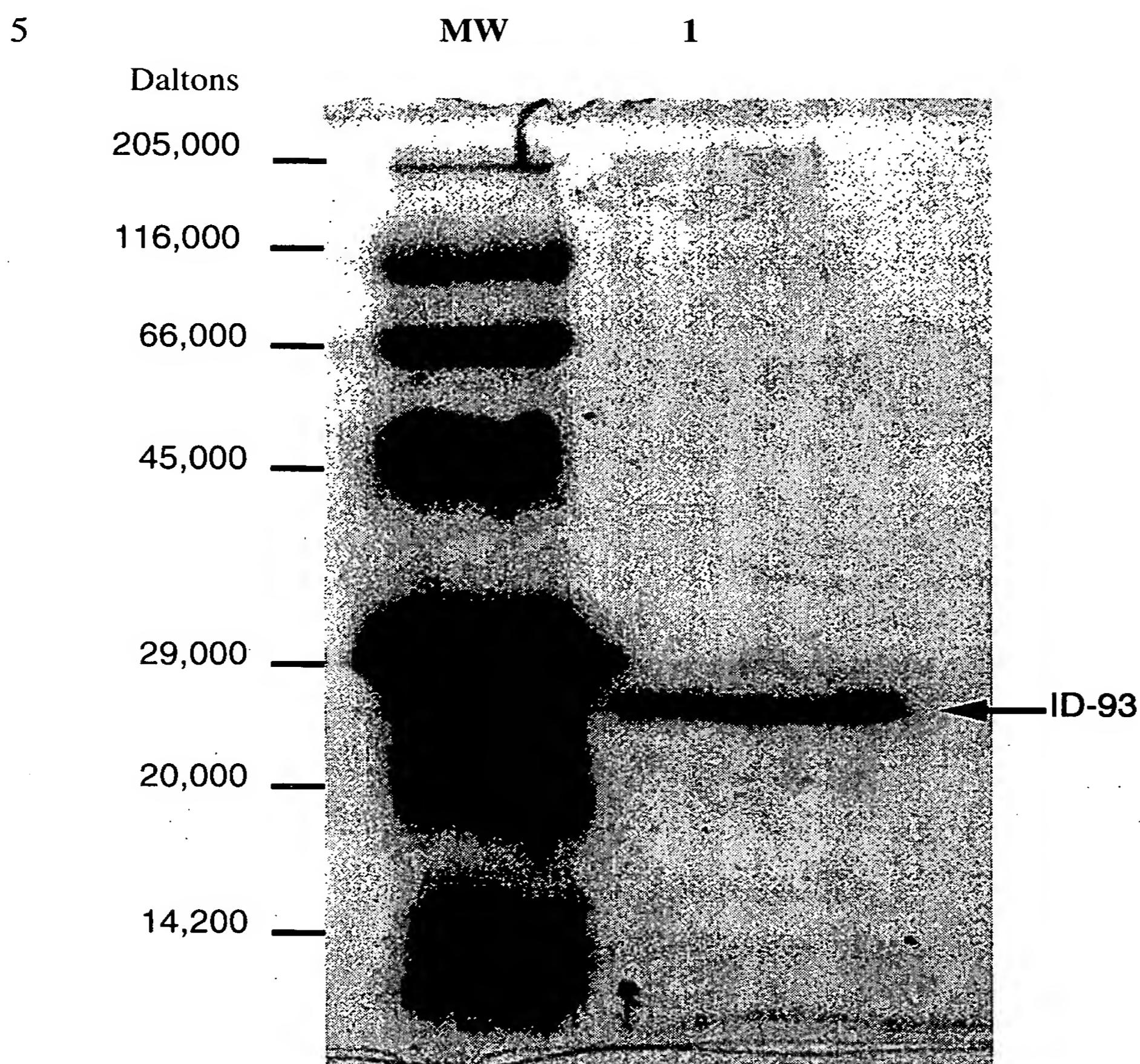




Figure 6

SDS-PAGE analysis of the purified ID-93 antigen

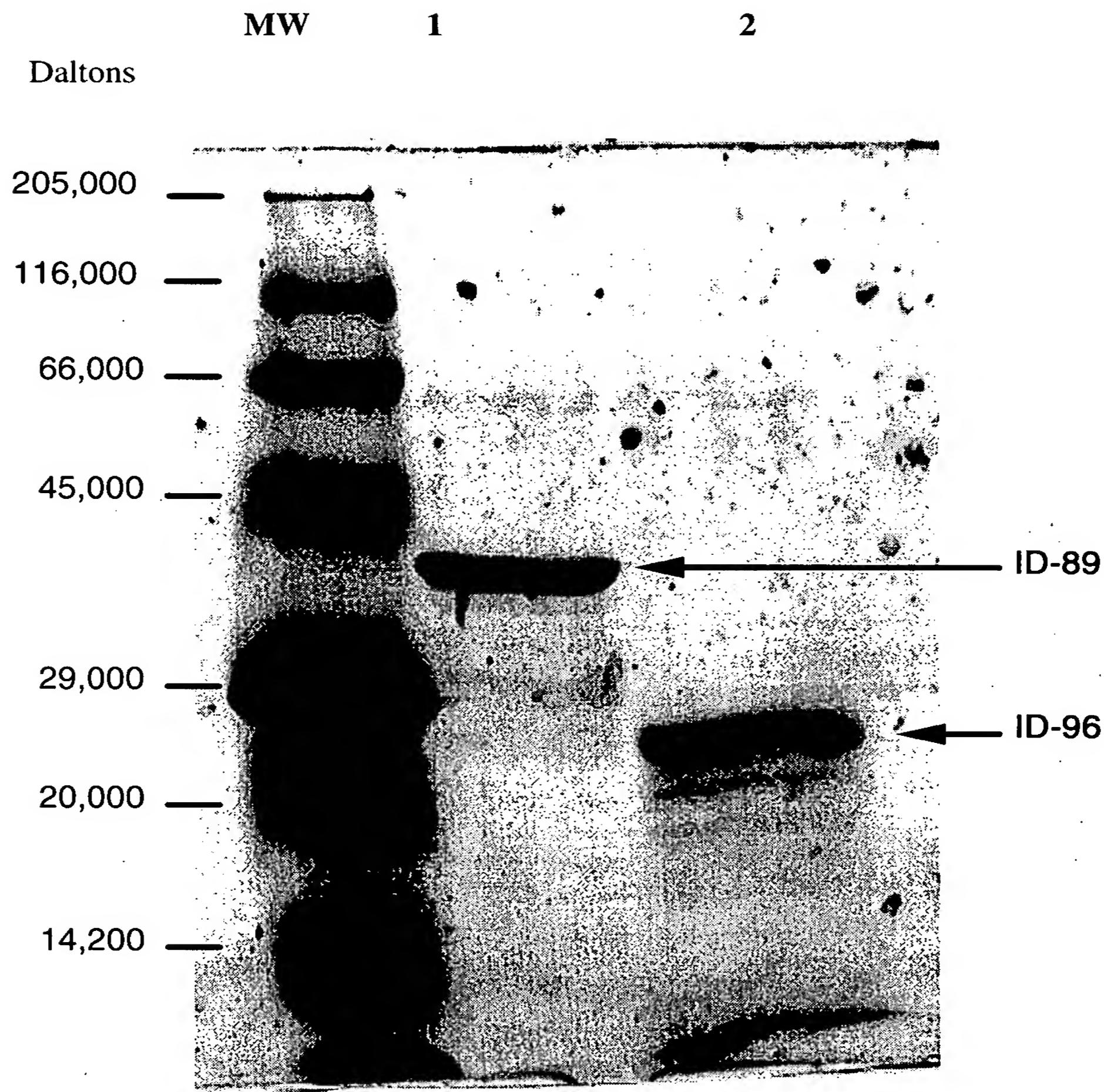




**Figure 7**

**SDS-PAGE analysis of the purified ID-89 and ID-96 protein antigens**

5



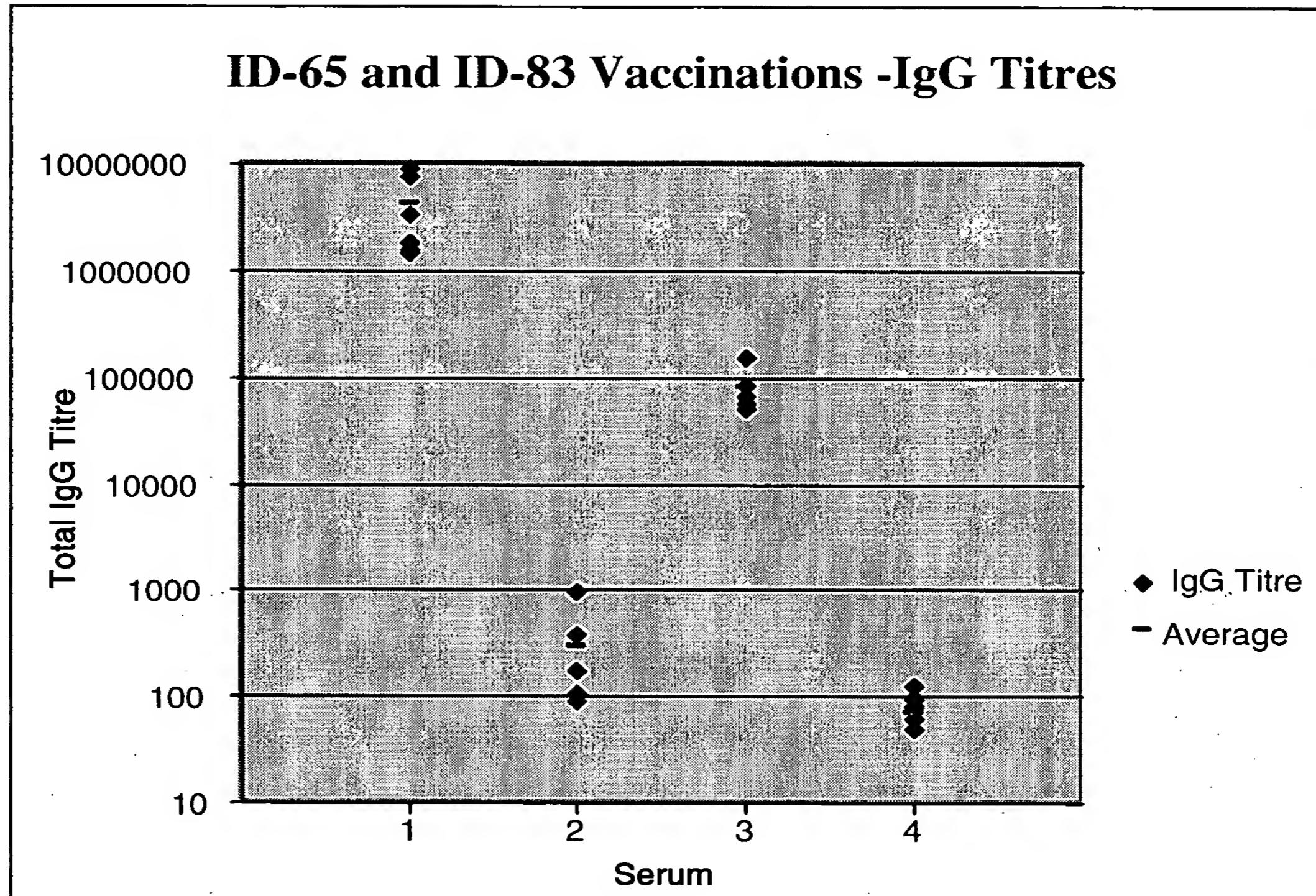
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Figure 8

IgG Titres against the ID-65 and ID-83 Proteins

5



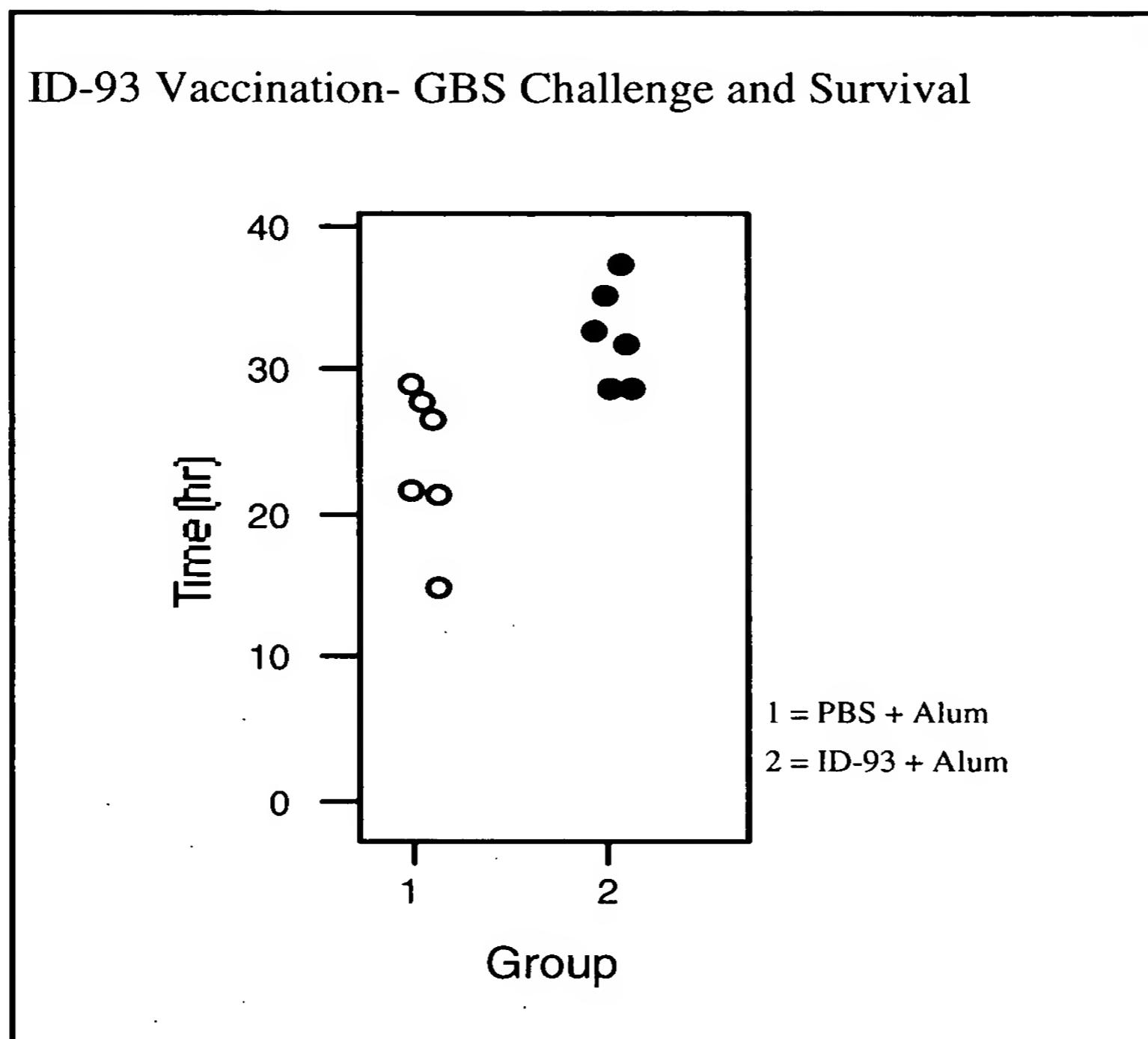
10

15



Figure 9

**Survival Data**



5

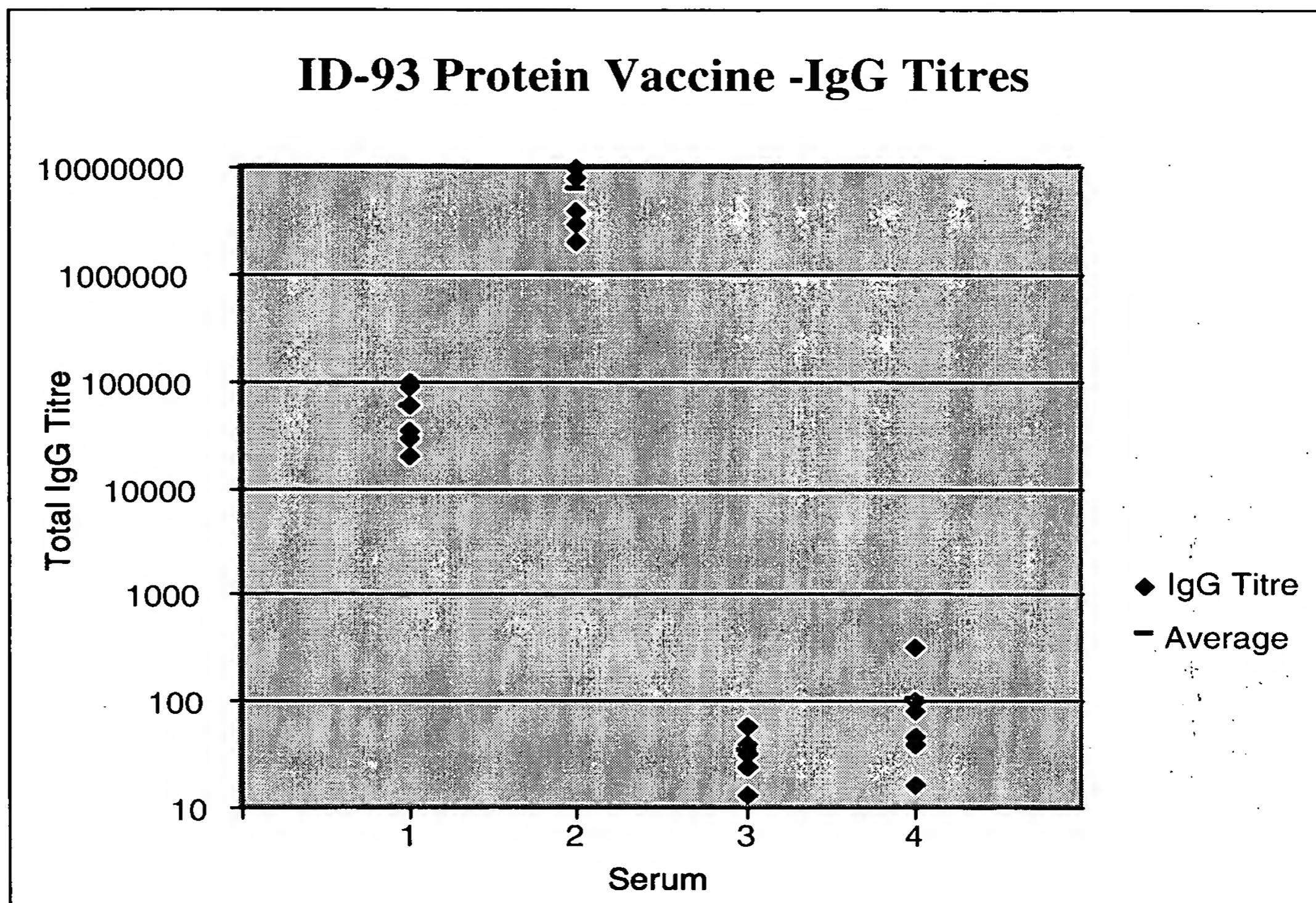
10



**Figure 10**

**IgG Titres against the ID-93 Protein**

5





**Figure 13      Southern blot analysis – ID-65**

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20  
5

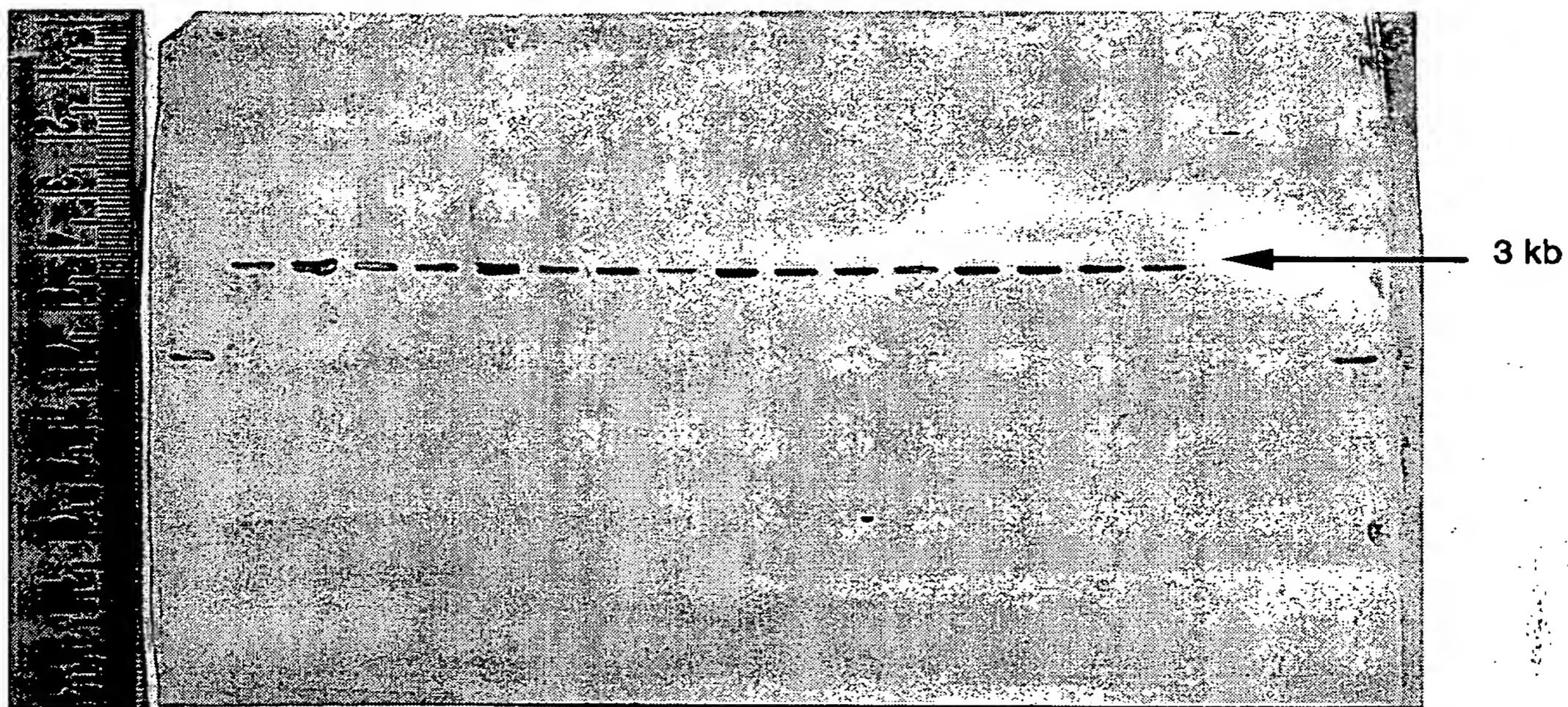


Figure 11

IgG Titres against the ID-89 and ID-96 Proteins

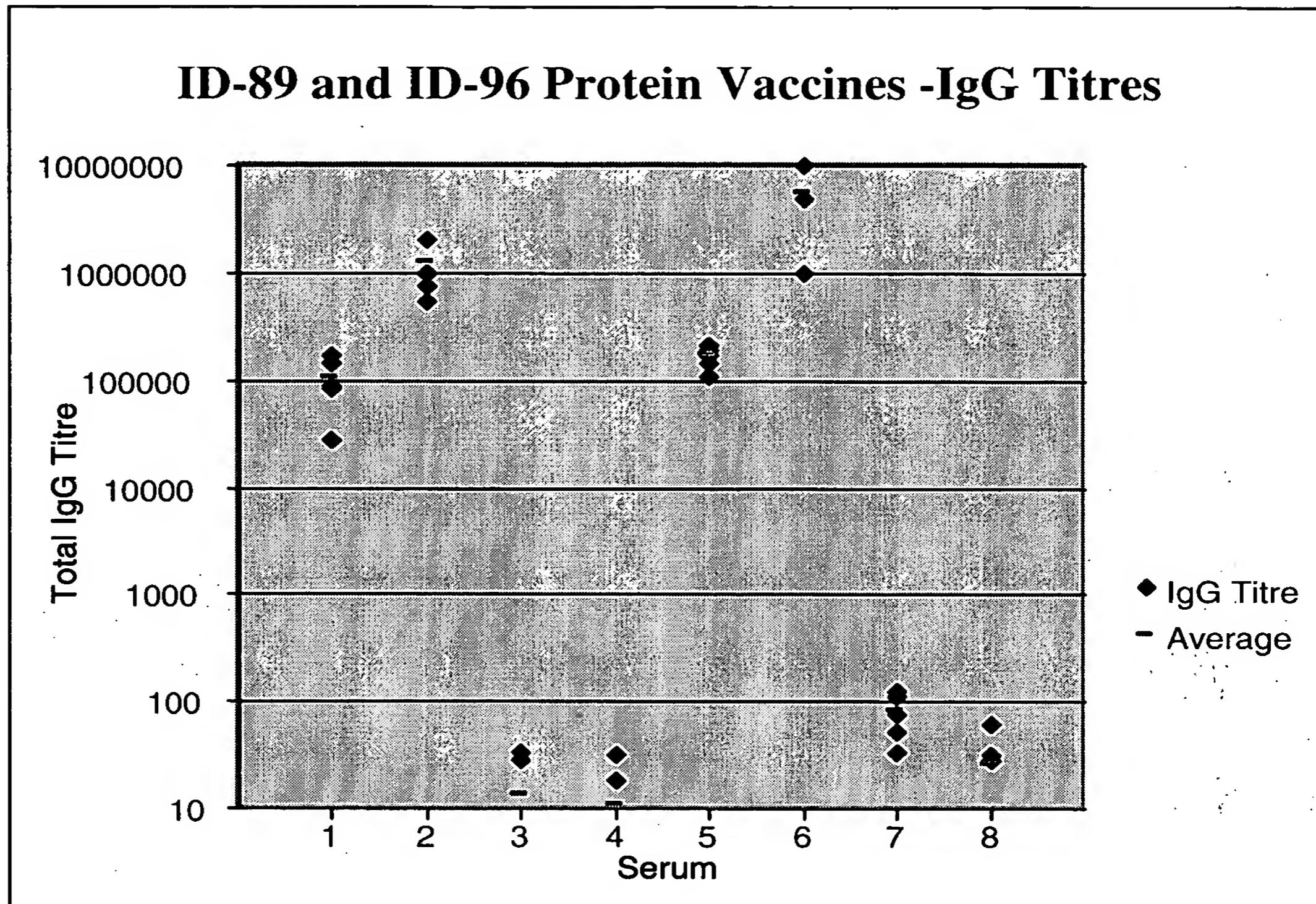




Figure 12

Southern blot analysis - *rib*

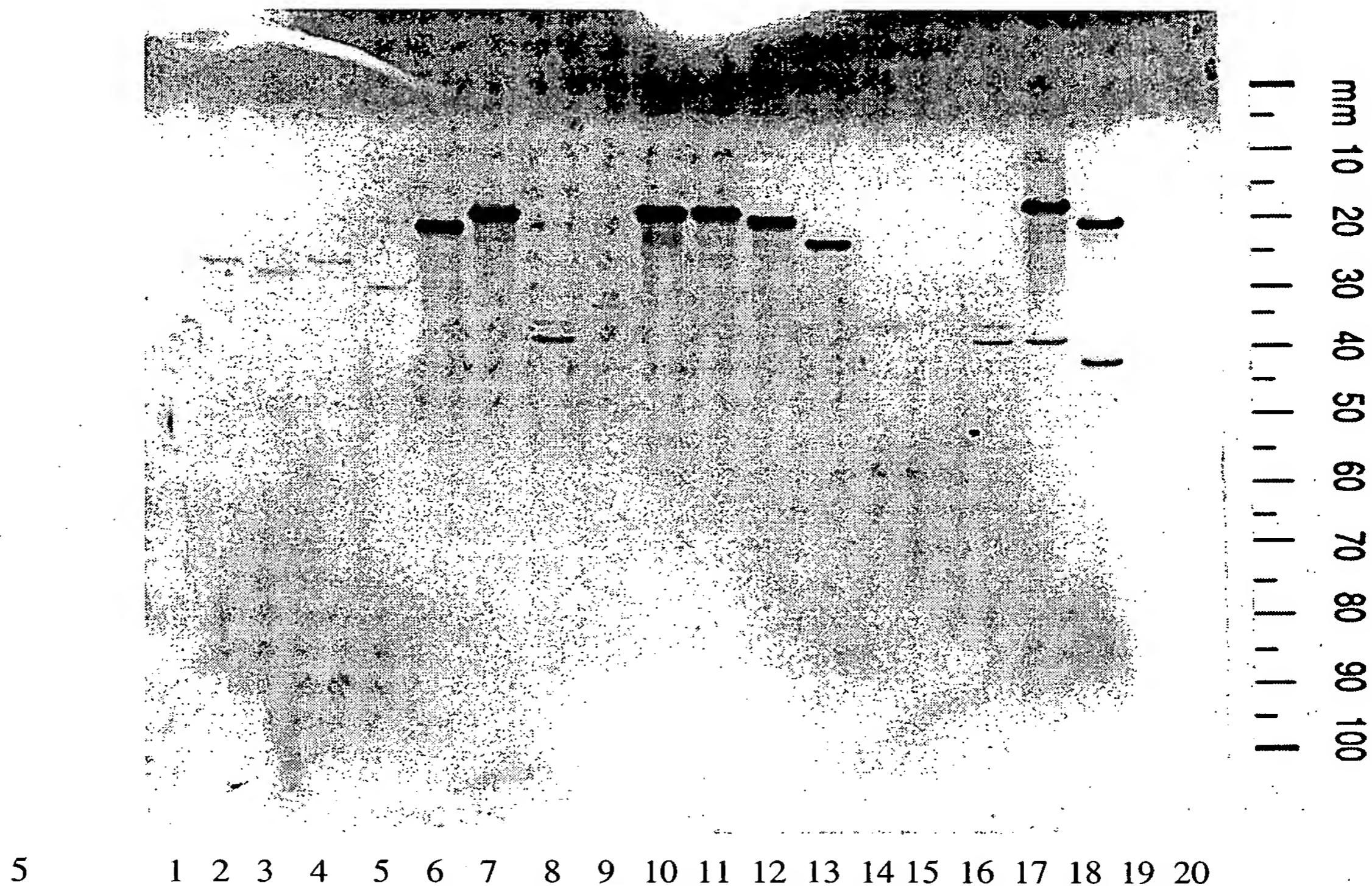
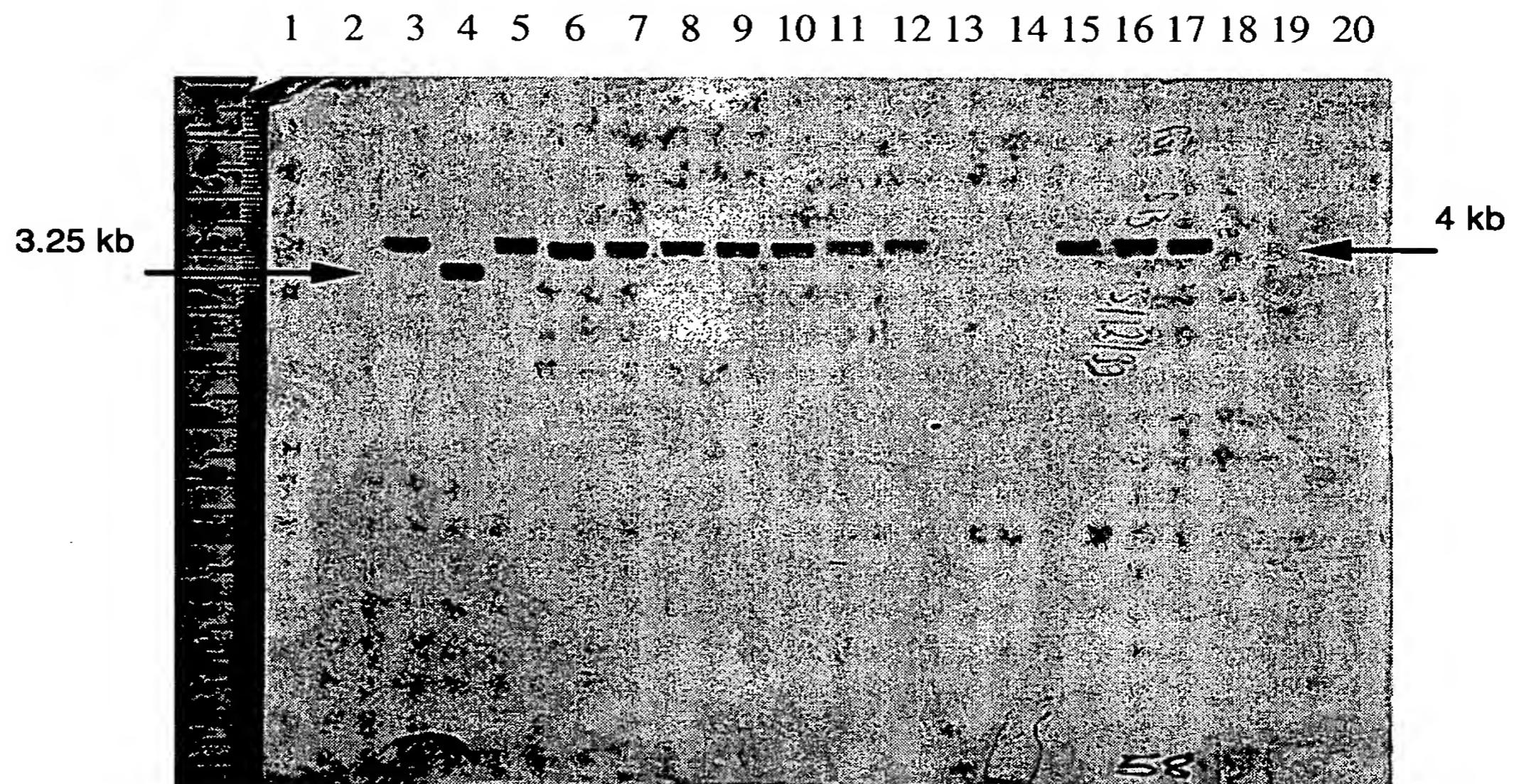




Figure 14

Southern blot analysis – ID-89



5

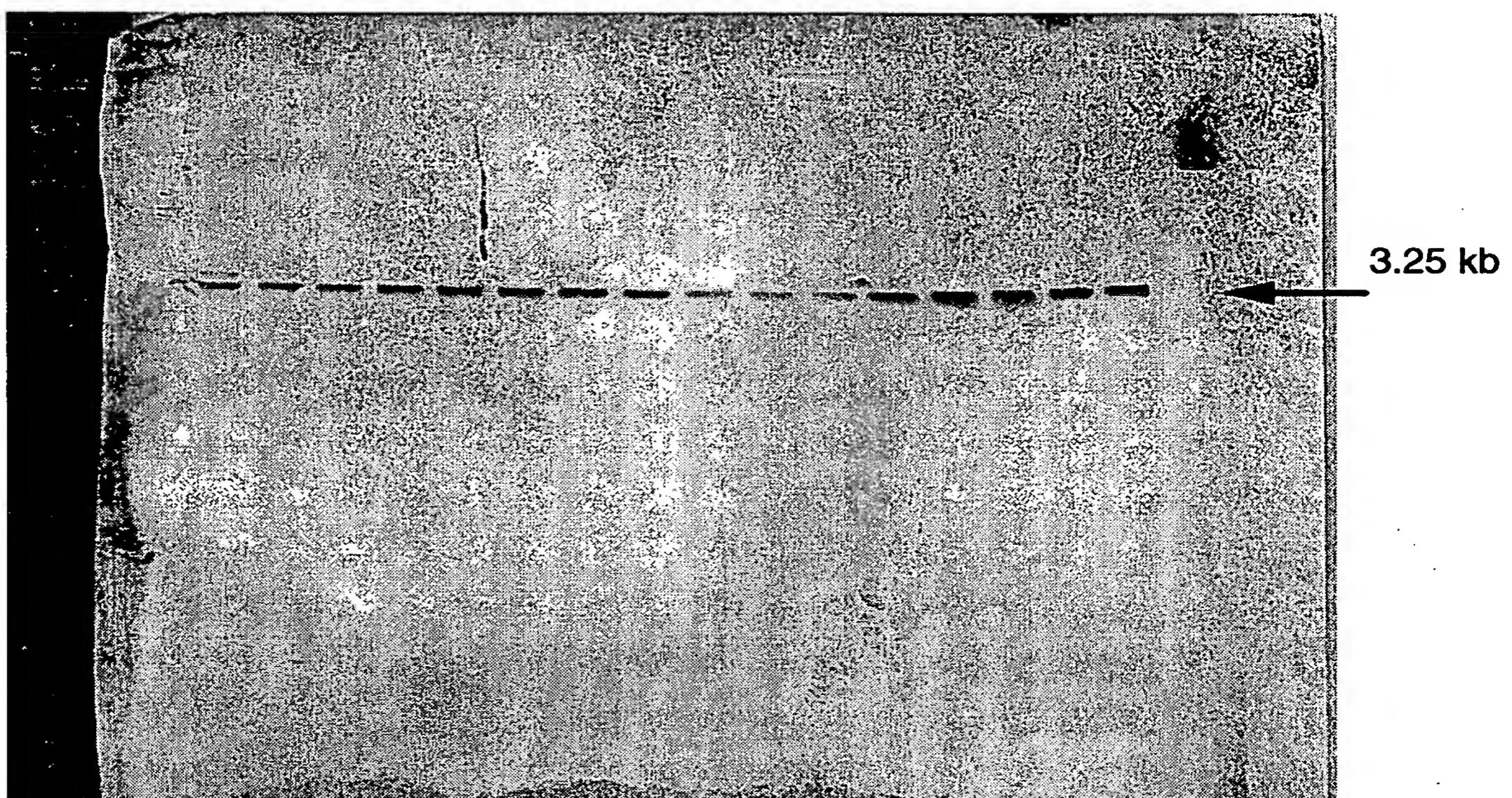


**Figure 15**

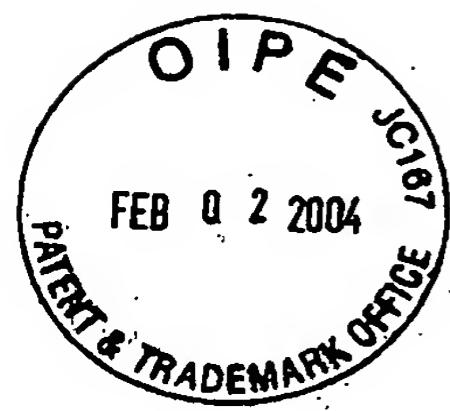
**Southern blot analysis – ID-93**

5

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20



10



**Figure 16                  Southern blot analysis – ID-96**

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20  
5

